

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE
REQUEST FOR FILING APPLICATION UNDER RULE 53(b)

08/15/00
170f

According to 37 CFR 1.53(b), please file a continuation/ divisional
pending prior PATENT APPLICATION of:

Inventor: **MAERTENS et al.**

No. 08/362,455

January 11, 1995

For NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES AND THEIR USE AS
THERAPEUTIC AND DIAGNOSTIC AGENTS

Assistant Commissioner for Patents

Washington, DC 20231

Sir:

This request for filing under Rule 53(b) is made by the following named inventor(s) (using the above-identified title):
Inventor(s): **MAERTENS et al.**

- Attached is a true copy of the prior application as originally filed including the specification, claims, Sequence Listing, Oath/Declaration and drawings (if any) and abstract (if any). No amendments (if any) referenced in the Oath or Declaration filed to complete the prior application introduced new matter.
- Priority is hereby claimed under 35 USC 119 based on the following foreign applications, the entire content of which is hereby incorporated by reference in this application:

Application Number

93.401 099.2

93.402.019.9

PCT/EP94/01323

certified copy(ies) of foreign application(s) attached or

already filed on _____ in prior appln. no. _____

already filed in PCT/EP94/01323

Country

Europe

Europe

International

Day/Month/Year/Filed

27/April/1993

05/August/1993

27/April/1994

filed

April 27, 1994

filed

- The prior application is assigned to N.V. INNOGENETICS S.A..
- Power of Attorney has been granted to Thomas E. Byrne et al, Reg. No. 32,205 of Nixon & Vanderhye P.C., 1100 N. Glebe Rd., 8th Flr, Arlington, VA 22201.
- Address all future communications to: Nixon & Vanderhye P.C., 1100 N. Glebe Rd., 8th Floor, Arlington, VA 22201.
- Please amend the specification by inserting before the first line --This is a continuation of application Serial No. 08/362,455, filed January 11, 1995, allowed, which is a 371 application of PCT/EP94/01323, filed April 27, 1994, the entire content of which is hereby incorporated by reference in this application.--
- Petition filed in prior application to extend its life to insure copendency.
- The Examiner's attention is directed to the prior art cited in the parent application by applicant and/or Examiner for the reasons stated therein and return of an initialed copy of the attached PTO-1449 Form listing same, pursuant to MPEP §609, are requested.
- Please enter the attached and/or below preliminary amendment prior to calculation of filing fee:

ATTACHED

- The entire disclosure of the prior application above-referenced is considered as being part of the disclosure of this new application and is hereby incorporated by reference therein.

FILING FEE IS BASED ON CLAIMS AS FILED LESS ANY HEREWITH CANCELED

Basic Filing Fee		\$	690.00
Total effective claims 23 - 20 (at least 20) =	3	x \$ 18.00	\$ 54.00
Independent claims 1 - 3 (at least 3) =	0	x \$ 78.00	\$ 0.00
If any proper multiple dependent claims now added for first time, add \$260.00 (ignore improper)			\$ 0.00
		SUBTOTAL	\$ 744.00
If "small entity," then enter half (1/2) of subtotal and subtract			-\$(0.00)
Assignment Recording Fee (\$40.00)			SECOND SUBTOTAL \$ 744.00
			\$ 0.00
		TOTAL FEE ENCLOSED	\$ 744.00

- Any future submission requiring an extension of time is hereby stated to include a petition for such time extension. The Commissioner is hereby authorized to charge any deficiency in the fee(s) filed, or asserted to be filed, or which should have been filed herewith (or with any paper hereafter filed in this application by this firm) to our Account No. 14-1140. A duplicate copy of this sheet is attached.

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NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES AND THEIR USE AS THERAPEUTIC AND DIAGNOSTIC AGENTS

The invention relates to new sequences of hepatitis C virus (HCV) genotypes and their use as therapeutic and diagnostic agents.

The present invention relates to new nucleotide and amino acid sequences corresponding to the coding region of a new type 2 subtype 2d, type-specific sequences corresponding to HCV type 3a, to new sequences corresponding to the coding region of a new subtype 3c, and to new sequences corresponding to the coding region of HCV type 4 and type 5 subtype 5a; a process for preparing them, and their use for diagnosis, prophylaxis and therapy.

The technical problem underlying the present invention is to provide new type-specific sequences of the Core, the E1, the E2, the NS3, the NS4 and the NS5 regions of HCV type 4 and type 5, as well as of new variants of HCV types 2 and 3. These new HCV sequences are useful to diagnose the presence of type 2 and/or type 3 and/or type 4 and/or type 5 HCV genotypes in a biological sample. Moreover, the availability of these new type-specific sequences can increase the overall sensitivity of HCV detection and should also prove to be useful for therapeutic purposes.

Hepatitis C viruses (HCV) have been found to be the major cause of non-A, non-B hepatitis. The sequences of cDNA clones covering the complete genome of several prototype isolates have been determined (Kato et al., 1990; Choo et al., 1991; Okamoto et al., 1991; Okamoto et al., 1992). Comparison of these isolates shows that the variability in nucleotide sequences can be used to distinguish at least 2 different genotypes, type 1 (HCV-1 and HCV-J) and type 2 (HC-J6 and HC-J8), with an average homology of about 68%. Within each type, at least two subtypes exist (e.g. represented by HCV-1 and HCV-J), having an average homology of about 79%. HCV genomes belonging to the same subtype show average homologies of more than 90% (Okamoto et al., 1992). However, the partial nucleotide sequence of the NS5 region of the HCV-T isolates showed at most 67% homology with the previously published sequences, indicating the existence of a yet another HCV type (Mori et al., 1992). Parts of the 5' untranslated region (UR), core, NS3, and NS5 regions of this type 3 have been published, further establishing the similar evolutionary distances between the 3 major genotypes and their subtypes (Chan et al., 1992).

The identification of type 3 genotypes in clinical samples can be achieved by means of PCR with type-specific primers for the NS5 region. However, the degree to which this will

be successful is largely dependent on sequence variability and on the virus titer present in the serum. Therefore, routine PCR in the open reading frame, especially for type 3 and the new type 4 and 5 described in the present invention and/or group V (Cha et al., 1992) genotypes can be predicted to be unsuccessful. A new typing system (LiPA), based on variation in the highly conserved 5' UR, proved to be more useful because the 5 major HCV genotypes and their subtypes can be determined (Stuyver et al., 1993). The selection of high-titer isolates enables to obtain PCR fragments for cloning with only 2 primers, while nested PCR requires that 4 primers match the unknown sequences of the new type 3, 4 and 5 genotypes.

New sequences of the 5' untranslated region (5'UR) have been listed by Bukh et al. (1992). For some of these, the E1 region has recently been described (Bukh et al., 1993). Isolates with similar sequences in the 5'UR to a group of isolates including DK12 and HK10 described by Bukh et al. (1992) and E-b1 to E-b8 described and classified as type 3 by Chan et al. (1991), have been reported and described in the 5'UR, the carboxyterminal part of E1, and in the NSS region as group IV by Cha et al. (1992; WO 92/19743), and have also been described in the 5'UR for isolate BR56 and classified as type 3 by the inventors of this application (Stuyver et al., 1993).

The aim of the present invention is to provide new HCV nucleotide and amino acid sequences enabling the detection of HCV infection.

Another aim of the present invention is to provide new nucleotide and amino acid HCV sequences enabling the classification of infected biological fluids into different serological groups unambiguously linked to types and subtypes at the genome level.

Another aim of the present invention is to provide new nucleotide and amino acid HCV sequences ameliorating the overall HCV detection rate.

Another aim of the present invention is to provide new HCV sequences, useful for the design of HCV vaccine compositions.

Another aim of the present invention is to provide a pharmaceutical composition consisting of antibodies raised against the polypeptides encoded by these new HCV sequences, for therapy or diagnosis.

The present invention relates more particularly to a composition comprising or consisting of at least one polynucleic acid containing at least 5, and preferably 8 or more contiguous nucleotides selected from at least one of the following HCV sequences:

- an HCV type 3 genomic sequence, more particularly in any of the following regions:

- the region spanning positions 417 to 957 of the Core/E1 region of HCV subtype 3a,
- the region spanning positions 4664 to 4730 of the NS3 region of HCV type 3,
- the region spanning positions 4892 to 5292 of the NS3/4 region of HCV type 3,
- the region spanning positions 8023 to 8235 of the NS5 region of the BR36 subgroup of HCV subtype 3a,
- an HCV subtype 3c genomic sequence,

more particularly the coding regions of the above-specified regions;

- an HCV subtype 2d genomic sequence, more particularly the coding region of HCV subtype 2d;
- an HCV type 4 genomic sequence, more particularly the coding region, more particularly the coding region of subtypes 4a, 4e, 4f, 4g, 4h, 4i, and 4j.
- an HCV type 5 genomic sequence, more particularly the coding region of HCV type 5, more particularly the regions encoding Core, E1, E2, NS3, and NS4 with said nucleotide numbering being with respect to the numbering of HCV nucleic acids as shown in Table 1, and with said polynucleic acids containing at least one nucleotide difference with known HCV (type 1, type 2, and type 3) polynucleic acid sequences in the above-indicated regions, or the complement thereof.

It is to be noted that the nucleotide difference in the polynucleic acids of the invention may involve or not an amino acid difference in the corresponding amino acid sequences coded by said polynucleic acids.

According to a preferred embodiment, the present invention relates to a composition comprising or containing at least one polynucleic acid encoding an HCV polyprotein, with said polynucleic acid containing at least 5, preferably at least 8 nucleotides corresponding to at least part of an HCV nucleotide sequence encoding an HCV polyprotein, and with said HCV polyprotein containing in its sequence at least one of the following amino acid residues: L7, Q43, M44, S60, R67, Q70, T71, A79, A87, N106, K115, A127, A190, S130, V134, G142, I144, E152, A157, V158, P165, S177 or Y177, I178, V180 or E180 or F182, R184, I186, H187, T189, A190, S191 or G191, Q192 or L192 or I192 or V192 or E192, N193 or H193 or P193, W194 or Y194, H195, A197 or I197 or V197 or T197, V202, I203 or L203, Q208, A210, V212, F214, T216, R217 or D217 or E217 or V217, H218 or N218, H219 or

V219 or L219, L227 or I227, M231 or E231 or Q231, T232 or D232 or A232 or K232, Q235 or I235, A237 or T237, I242, I246, S247, S248, V249, S250 or Y250, I251 or V251 or M251 or F251, D252, T254 or V254, L255 or V255, E256 or A256, M258 or F258 or V258, A260 or Q260 or S260, A261, T264 or Y264, M265, I266 or A266, A267, G268 or T268, F271 or M271 or V271, I277, M280 or H280, I284 or A284 or L84, V274, V291, N292 or S292, R293 or I293 or Y293, Q294 or R294, L297 or I297 or Q297, A299 or K299 or Q299, N303 or T303, T308 or L308, T310 or F310 or A310 or D310 or V310, L313, G317 or Q317, L333, S351, A358, A359, A363, S364, A366, T369, L373, F376, Q386, I387, S392, I399, F402, I403, R405, D454, A461, A463, T464, K484, Q500, E501, S521, K522, H524, N528, S531, S532, V534, F536, F537, M539, I546, C1282, A1283, H1310, V1312, Q1321, P1368, V1372, V1373, K1405, Q1406, S1409, A1424, A1429, C1435, S1436, S1456, H1496, A1504, D1510, D1529, I1543, N1567, D1556, N1567, M1572, Q1579, L1581, S1583, F1585, V1595, E1606 or T1606, M1611, V1612 or L1612, P1630, C1636, P1651, T1656 or I1656, L1663, V1667, V1677, A1681, H1685, E1687, G1689, V1695, A1700, Q1704, Y1705, A1713, A1714 or S1714, M1718, D1719, A1721 or T1721, R1722, A1723 or V1723, H1726 or G1726, E1730, V1732, F1735, I1736, S1737, R1738, T1739, G1740, Q1741, K1742, Q1743, A1744, T1745, L1746, E1747 or K1747, I1749, A1750, T1751 or A1751, V1753, N1755, K1756, A1757, P1758, A1759, H1762, T1763, Y1764, P2645, A2647, K2650, K2653 or L2653, S2664, N2673, F2680, K2681, L2686, H2692, Q2695 or L2695 or I2695, V2712, F2715, V2719 or Q2719, T2722, T2724, S2725, R2726, G2729, Y2735, H2739, I2748, G2746 or I2746, I2748, P2752 or K2752, P2754 or T2754, T2757 or P2757, with said notation being composed of a letter representing the amino acid residue by its one-letter code, and a number representing the amino acid numbering according to Kato et al., 1990.

Each of the above-mentioned residues can be found in any of Figures 2, 5, 7, 11 or 12 showing the new amino acid sequences of the present invention aligned with known sequences of other types or subtypes of HCV for the Core, E1, E2, NS3, NS4, and NS5 regions.

More particularly, a polynucleic acid contained in the composition according to the present invention contains at least 5, preferably 8, or more contiguous nucleotides corresponding to a sequence of contiguous nucleotides selected from at least one of HCV sequences encoding the following new HCV amino acid sequences:

- new sequences spanning amino acid positions 1 to 319 of the Core/E1 region of HCV subtype 2d, type 3 (more particularly new sequences for subtypes 3a and 3c), new type 4

subtypes (more particularly new sequences for subtypes 4a, 4e, 4f, 4g, 4h, 4i and 4j) and type 5a, as shown in Figure 5;

- new sequences spanning amino acid positions 328 to 546 of the E1/E2 region of HCV subtype 5a as shown in Figure 12;
- new sequences spanning amino acid positions 1556 to 1764 of the NS3/NS4 region of HCV type 3 (more particularly for new subtypes 3a sequences), and subtype 5a, as shown in Figure 7 or 11;
- new sequences spanning amino acid positions 2645 to 2757 of the NS5B region of HCV subtype 2d, type 3 (more particularly for new subtypes 3a and 3c), new type 4 subtypes (more particularly subtypes 4a, 4e, 4f, 4g, 4h, 4i and 4j) and subtype 5a, as shown in Figure 2,

Using the LiPA system mentioned above, Brazilian blood donors with high titer type 3 hepatitis C virus, Gabonese patients with high-titer type 4 hepatitis C virus, and a Belgian patient with high-titer HCV type 5 infection were selected. Nucleotide sequences in the core, E1, NS5 and NS4 regions which have not yet been reported before, were analyzed in the frame of the invention. Coding sequences (with the exception of the core region) of any type 4 isolate are reported for the first time in the present invention. The NS5b region was also analyzed for the new type 3 isolates. After having determined the NS5b sequences, comparison with the Ta and Tb subtypes described by Mori et al. (1992) was possible, and the type 3 sequences could be identified as type 3a genotypes. The new type 4 isolates segregated into 10 subtypes, based on homologies obtained in the NS5 and E1 regions. New type 2 and 3 sequences could also be distinguished from previously described type 2 or 3 subtypes from sera collected in Belgium and the Netherlands.

The term "polynucleic acid" refers to a single stranded or double stranded nucleic acid sequence which may contain at least 5 contiguous nucleotides to the complete nucleotide sequence (f.i. at least 6, 7, 8, 9, 10, 11, 12, 13, 14, 15 or more contiguous nucleotides). A polynucleic acid which is up till about 100 nucleotides in length is often also referred to as an oligonucleotide. A polynucleic acid may consist of deoxyribonucleotides or ribonucleotides, nucleotide analogues or modified nucleotides, or may have been adapted for therapeutic purposes. A polynucleic acid may also comprise a double stranded cDNA clone which can be used for cloning purposes, or for *in vivo* therapy, or prophylaxis.

The term "polynucleic acid composition" refers to any kind of composition comprising essentially said polynucleic acids. Said composition may be of a diagnostic or a therapeutic

nature.

The expression "nucleotides corresponding to" refers to nucleotides which are homologous or complementary to an indicated nucleotide sequence or region within a specific HCV sequence.

The term "coding region" corresponds to the region of the HCV genome that encodes the HCV polyprotein. In fact, it comprises the complete genome with the exception of the 5' untranslated region and 3' untranslated region.

The term "HCV polyprotein" refers to the HCV polyprotein of the HCV-J isolate (Kato et al., 1990). The adenine residue at position 330 (Kato et al., 1990) is the first residue of the ATG codon that initiates the long HCV polyprotein of 3010 amino acids in HCV-J and other type 1b isolates, and of 3011 amino acids in HCV-1 and other type 1a isolates, and of 3033 amino acids in type 2 isolates HC-J6 and HC-J8 (Okamoto et al., 1992).

This adenine is designated as position 1 at the nucleic acid level, and this methionine is designated as position 1 at the amino acid level, in the present invention. As type 1a isolates contain 1 extra amino acid in the NS5a region, coding sequences of type 1a and 1b have identical numbering in the Core, E1, NS3, and NS4 region, but will differ in the NS5b region as indicated in Table 1. Type 2 isolates have 4 extra amino acids in the E2 region, and 17 or 18 extra amino acids in

the NS5 region compared to type 1 isolates, and will differ in numbering from type 1 isolates in the NS3/4 region and NS5b regions as indicated in Table 1.

TABLE I

	Region	Positions described in the present invention*	Positions described for HCV-J (Kato et al., 1990)	Positions described for HCV-1 (Choo et al., 1991)	Positions described for HC-J6, HC-J8 (Okamoto et al., 1992)
Nucleotides	NS5b	8023/8235 7932/8271	8352/8564 8261/8600	8026/8238 7935/8274	8433/8645 8342/8681
	NS3/4	4664/5292 4664/4730 4892/5292 3856/4209 4936/5292	4993/5621 4993/5059 5221/5621 4185 4528 5265 5621	4664/5292 4664/4730 4892/5292 3856/4209 4936/5292	5017/5645 5017/5083 5245/5645 4209 4762 5289 5645
		coding region of present invention	330-9359	1/9033	342-9439
Amino Acids	NS5b	2675/2745 2645/2757	2675/2745 2645/2757	2676/2746 2646/2758	2698/2768 2668/2780
	NS3/4	1556/1764 1286/1403 1646/1764	1556/1764 1286/1403 1646/1764	1556/1764 1286/1403 1646/1764	1560/1768 1290/1407 1650/1768

Table 1 Comparison of the HCV nucleotide and amino acid numbering system used in the present invention (*) with the numbering used for other prototype isolates. For example, 8352/8564 indicates the region designated by the numbering from nucleotide 8352 to nucleotide 8564 as described by Kato et al (1990). Since the numbering system of the present invention starts at the polyprotein initiation site, the 329 nucleotides of the 5' untranslated region described by Kato et al (1990) have to be subtracted, and the corresponding region is numbered from nucleotide 8023 ("8352-329") to 8235 ("8564-329")

The term "HCV type" corresponds to a group of HCV isolates of which the complete genome shows more than 74% homology at the nucleic acid level, or of which the NS5 region between nucleotide positions 7932 and 8271 shows more than 74% homology at the nucleic acid level, or of which the complete HCV polyprotein shows more than 78% homology at the amino acid level, or of which the NS5 region between amino acids at positions 2645 and 2757 shows more than 80% homology at the amino acid level, to polyproteins of the other isolates of the group, with said numbering beginning at the first ATG codon or first methionine of the long HCV polyprotein of the HCV-J isolate (Kato et al., 1990). Isolates belonging to different types of HCV exhibit homologies, over the complete genome, of less than 74% at the nucleic acid level and less than 78% at the amino acid level. Isolates belonging to the same type usually show homologies of about 92 to 95% at the nucleic acid level and 95 to 96% at the amino acid level when belonging to the same subtype, and those belonging to the same type but different subtypes preferably show homologies of about 79% at the nucleic acid level and 85-86% at the amino acid level.

More preferably the definition of HCV types is concluded from the classification of HCV isolates according to their nucleotide distances calculated as detailed below:

(1) based on phylogenetic analysis of nucleic acid sequences in the NS5b region between nucleotides 7935 and 8274 (Choo et al., 1991) or 8261 and 8600 (Kato et al., 1990) or 8342 and 8681 (Okamoto et al., 1991), isolates belonging to the same HCV type show nucleotide distances of less than 0.34, usually less than 0.33, and more usually of less than 0.32, and isolates belonging to the same subtype show nucleotide distances of less than 0.135, usually of less than 0.13, and more usually of less than 0.125, and consequently isolates belonging to the same type but different subtypes show nucleotide distances ranging from 0.135 to 0.34, usually ranging from 0.1384 to 0.2477, and more usually ranging from 0.15 to 0.32, and isolates belonging to different HCV types show nucleotide distances greater than 0.34, usually greater than 0.35, and more usually of greater than 0.358, more usually ranging from 0.1384 to 0.2977.

(2) based on phylogenetic analysis of nucleic acid sequences in the core/E1 region between nucleotides 378 and 957, isolates belonging to the same HCV type show nucleotide distances of less than 0.38, usually of less than 0.37, and more usually of less than 0.364, and isolates belonging to the same subtype show nucleotide distances of less than 0.17, usually of less than 0.16, and more usually of less than 0.15, more usually less than 0.135, more usually less than 0.134, and consequently isolates belonging to the same type but different subtypes show

nucleotide distances ranging from 0.15 to 0.38, usually ranging from 0.16 to 0.37, and more usually ranging from 0.17 to 0.36, more usually ranging from 0.133 to 0.379, and isolates belonging to different HCV types show nucleotide distances greater than 0.34, 0.35, 0.36, usually more than 0.365, and more usually of greater than 0.37,

(3) based on phylogenetic analysis of nucleic acid sequences in the NS3/NS4 region between nucleotides 4664 and 5292 (Choo et al., 1991) or between nucleotides 4993 and 5621 (Kato et al., 1990) or between nucleotides 5017 and 5645 (Okamoto et al., 1991), isolates belonging to the same HCV type show nucleotide distances of less than 0.35, usually of less than 0.34, and more usually of less than 0.33, and isolates belonging to the same subtype show nucleotide distances of less than 0.19, usually of less than 0.18, and more usually of less than 0.17, and consequently isolates belonging to the same type but different subtypes show nucleotide distances ranging from 0.17 to 0.35, usually ranging from 0.18 to 0.34, and more usually ranging from 0.19 to 0.33, and isolates belonging to different HCV types show nucleotide distances greater than 0.33, usually greater than 0.34, and more usually of greater than 0.35.

Table 2 : Molecular evolutionary distances

Region	Core/E1 579 bp	E1 384 bp	NSSB 340 bp	NSSB 222 bp
Isolates*	0.0017 - 0.1347 (0.0750 ± 0.0245)	0.0026 - 0.2031 (0.0969 ± 0.0289)	0.0003 - 0.1151 (0.0637 ± 0.0229)	0.000 - 0.1323 (0.0607 ± 0.0205)
Subtypes*	0.1330 - 0.3794 (0.2786 ± 0.0363)	0.1645 - 0.4869 (0.3761 ± 0.0433)	0.1384 - 0.2977 (0.2219 ± 0.0341)	0.117 - 0.3538 (0.2391 ± 0.0399)
Types*	0.3479 - 0.6306 (0.4703 ± 0.0525)	0.4309 - 0.9561 (0.6308 ± 0.0928)	0.3581 - 0.6670 (0.4994 ± 0.0495)	0.3457 - 0.7471 (0.5295 ± 0.0627)

- Figures created by the PHYLIP program DNADIST are expressed as minimum to maximum (average ± standard deviation). Phylogenetic distances for isolates belonging to the same subtype ('isolates'), to different subtypes of the same type ('subtypes'), and to different types ('types') are given.

In a comparative phylogenetic analysis of available sequences, ranges of molecular evolutionary distances for different regions of the genome were calculated, based on 19,781

pairwise comparisons by means of the DNA DIST program of the phylogeny inference package PHYLIP version 3.5C (Felsenstein, 1993). The results are shown in Table 2 and indicate that although the majority of distances obtained in each region fit with classification of a certain isolate, only the ranges obtained in the 340bp NS5B-region are non-overlapping and therefore conclusive. However, as was performed in the present invention, it is preferable to obtain sequence information from at least 2 regions before final classification of a given isolate.

Designation of a number to the different types of HCV and HCV types nomenclature is based on chronological discovery of the different types. The numbering system used in the present invention might still fluctuate according to international conventions or guidelines. For example, "type 4" might be changed into "type 5" or "type 6".

The term "subtype" corresponds to a group of HCV isolates of which the complete polyprotein shows a homology of more than 90% both at the nucleic acid and amino acid levels, or of which the NS5 region between nucleotide positions 7932 and 8271 shows a homology of more than 90% at the nucleic acid level to the corresponding parts of the genomes of the other isolates of the same group, with said numbering beginning with the adenine residue of the initiation codon of the HCV polyprotein. Isolates belonging to the same type but different subtypes of HCV show homologies of more than 74% at the nucleic acid level and of more than 78% at the amino acid level.

The term "BR36 subgroup" refers to a group of type 3a HCV isolates (BR36, BR33, BR34) that are 95 %, preferably 95.5 %, most preferably 96 % homologous to the sequences as represented in SEQ ID NO 1, 3, 5, 7, 9, 11 in the NS5b region from position 8023 to 8235.

It is to be understood that extremely variable regions like the E1, E2 and NS4 regions will exhibit lower homologies than the average homology of the complete genome of the polyprotein.

Using these criteria, HCV isolates can be classified into at least 6 types. Several subtypes can clearly be distinguished in types 1, 2, 3 and 4 : 1a, 1b, 2a, 2b, 2c, 2d, 3a, 3b, 4a, 4b, 4c, 4d, 4e, 4f, 4g, 4h, 4i and 4j based on homologies of the 5' UR and coding regions including the part of NS5 between positions 7932 and 8271. An overview of most of the reported isolates and their proposed classification according to the typing system of the present invention as well as other proposed classifications is presented in Table 3.

Table 3

HCV CLASSIFICATION

	OKA-MOTO	MORI	NAKA O	CHA	PROTOTYPE
1a	I	I	Pt	GI	HCV-1, HCV-H, HC-J1
1b	II	II	KI	GII	HCV-J, HCV-BK, HCV-T, HC-JK1, HC-J4, HCV-CHINA
1c					HC-G9
2a	III	III	K2a	GIII	HC-J6
2b	IV	IV	K2b	GIII	HC-J8
2c					S83, ARG6, ARG8, I10, T983
2d					NE92
3a	V	V	K3	GIV	E-b1, Ta, BR36, BR33, HD10, NZL1
3b		VI	K3	GIV	HCV-TR, Tb
3c					BE98
4a					Z4, GB809-4
4b					Z1
4c					GB116, GB358, GB215, Z6, Z7
4d					DK13
4e					GB809-1, CAM600, CAM736
4f					CAM622, CAM627
4g					GB549
4h					GB438
4i					CAR4/1205
4j					CAR1/501
4k					EG29
5a			GV		SA3, SA4, SA1, SA7, SA11, BE95
6a					HK1, HK2, HK3, HK4

The term "complement" refers to a nucleotide sequence which is complementary to an indicated sequence and which is able to hybridize to the indicated sequences.

The composition of the invention can comprise many combinations. By way of example, the composition of the invention can comprise:

- two (or more) nucleic acids from the same region or,
- two nucleic acids (or more), respectively from different regions, for the same isolate or for different isolates,
- or nucleic acids from the same regions and from at least two different regions (for the same isolate or for different isolates).

The present invention relates more particularly to a polynucleic acid composition as defined above, wherein said polynucleic acid corresponds to a nucleotide sequence selected from any of the following HCV type 3 genomic sequences:

- an HCV genomic sequence having a homology of at least 67%, preferably more than 69%, more preferably 71%, even more preferably more than 73%, or most preferably more than 76% to any of the sequences as represented in SEQ ID NO 13, 15, 17, 19, 21, 23, 25 or 27 (HD10, BR36 or BR33 sequences) in the region spanning positions 417 to 957 of the Core/E1 region as shown in Figure 4;
- an HCV genomic sequence having a homology of at least 65%, preferably more than 67%, preferably more than 69%, even more preferably more than 70%, most preferably more than 74% to any of the sequences as represented in SEQ ID NO 13, 15, 17, 19, 21, 23, 25 or 27 (HD10, BR36 or BR33 sequences) in the region spanning positions 574 to 957 of the E1 region as shown in Figure 4;
- an HCV genomic sequence as having a homology of at least 79%, more preferably at least 81%, most preferably more than 83% or more to any of the sequences as represented in SEQ ID NO 147 (representing positions 1 to 346 of the Core region of HVC type 3c, sequence BE98) in the region spanning positions 1 to 378 of the Core region as shown in Figure 3;
- an HCV genomic sequence of HVC type 3a having a homology of at least 74%, more preferably at least 76%, most preferably more than 78% or more to any of the sequences as represented in SEQ ID NO 13, 15, 17, 19, 21, 23, 25 or 27 (HD10, BR36 or BR33 sequences) in the region spanning positions 417 to 957 in the Core/E1 region as shown in Figure 4;
- an HCV genomic sequence of HCV type 3a as having a homology of at least 74%,

preferably more than 76%, most preferably 78% or more to any of the sequences as represented in SEQ ID NO 13, 15, 17, 19, 21, 23, 25 or 27 (HD10, BR36 or BR33 sequences) in the region spanning positions 574 to 957 in the E1 region as shown in Figure 4;

- an HCV genomic sequence as having a homology of more than 73.5%, preferably more than 74%, most preferably 75% homology to the sequence as represented in SEQ ID NO 29 (HCC153 sequence) in the region spanning positions 4664 to 4730 of the NS3 region as shown in figure 6;
- an HCV genomic sequence having a homology of more than 70%, preferably more than 72%, most preferably more than 74% homology to any of the sequences as represented in SEQ ID NO 29, 31, 33, 35, 37 or 39 (HCC153, HD10, BR36 sequences) in the region spanning positions 4892 to 5292 in the NS3/NS4 region as shown in Figure 6 or 10;
- an HCV genomic sequence of the BR36 subgroup of HCV type 3a as having a homology of more than 95%, preferably 95.5%, most preferabiy 96% homology to any of the sequences as represented in SEQ ID NO 5, 7, 1, 3, 9 or 11 (BR34, BR33, BR36 sequences) in the region spanning positions 8023 to 8235 of the NS5 region as shown in Figure 1;
- an HCV genomic sequence of the BR36 subgroup of HCV type 3a as having a homology of more than 96%, preferably 96.5%, most preferably 97% homology to any of the sequences as represented in SEQ ID NO 5, 7, 1, 3, 9 or 11 (BR34, BR33, BR36 sequences) in the region spanning positions 8023 to 8192 of the NS5B region as shown in Figure 1;
- an HCV genomic sequence of HCV type 3c being characterized as having a homology of more than 79%, more preferably more than 81%, and most preferably more than 83% to the sequence as represented in SEQ ID NO 149 (BE98 sequence) in the region spanning positions 7932 to 8271 in the NS5B region as shown in Figure 1.

Preferentially the above-mentioned genomic HCV sequences depict sequences from the coding regions of all the above-mentioned sequences.

According to the nucleotide distance classification system (with said nucleotide distances being calculated as explained above), said sequences of said composition are selected from:

- an HCV genomic sequence being characterized as having a nucleotide distance of less than 0.44, preferably of less than 0.40, most preferably of less than 0.36 to any of the sequences as represented in SEQ ID NO 13, 15, 17, 19, 21, 23, 25 or 27 in the region

spanning positions 417 to 957 of the Core/E1 region as shown in Figure 4;

- an HCV genomic sequence being characterized having a nucleotide distance of less than 0.53, preferably less than 0.49, most preferably of less than 0.45 to any of the sequences as represented in SEQ ID NO 19, 21, 23, 25 or 27 in the region spanning positions 574 to 957 of the E1 region as shown in Figure 4;
- an HCV genomic sequence characterized having a nucleotide distance of less than 0.15, preferably less than 0.13, and most preferably less than 0.11 to any of the sequences as represented in SEQ ID NO 147 in the region spanning positions 1 to 378 of the Core region as shown in Figure 3;
- an HCV genomic sequence of HVC type 3a being characterized as having a nucleotide distance of less than 0.3, preferably less than 0.26, most preferably of less than 0.22 to any of the sequences as represented in SEQ ID NO 13, 15, 17, 19, 21, 23, 25 or 27 in the region spanning positions 417 to 957 in the Core/E1 region as shown in Figure 4;
- an HCV genomic sequence of HCV type 3a being characterized as having a nucleotide distance of less than 0.35, preferably less than 0.31, most preferably of less than 0.27 to any of the sequences as represented in SEQ ID NO 13, 15, 17, 19, 21, 23, 25 or 27 in the region spanning positions 574 to 957 in the E1 region as shown in Figure 4;
- an HCV genomic sequence of the BR36 subgroup of HCV type 3a being characterized as having a nucleotide sequence of less than 0.0423, preferably less than 0.042, preferably less than 0.0362 to any of the sequences as represented in SEQ ID NO 5, 7, 1, 3, 9 or 11 in the region spanning positions 8023 to 8235 of the NS5 region as shown in Figure 1;
- an HCV genomic sequence of HCV type 3c being characterized as having a nucleotide distance of less than 0.255, preferably of less than 0.25, more preferably of less than 0.21, most preferably of less than 0.17 to the sequence as represented in SEQ ID NO 149 in the region spanning positions 7932 to 8271 in the NS5B region as shown in Figure 1.

In the present application, the E1 sequences encoding the antigenic ectodomain of the E1 protein, which does not overlap the carboxyterminal signal-anchor sequences of E1 disclosed by Cha et al. (1992; WO 92/19743), in addition to the NS4 epitope region, and a part of the NS5 region are disclosed for 4 different isolates: BR33, BR34, BR36, HCCI53 and HD10, all belonging to type 3a (SEQ ID NO 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 35, 37 or 39).

Also within the present invention are new subtype 3c sequences (SEQ ID NO 147, 149 of the isolate BE98 in the Core and NS5 regions (see Figures 3 and 1).

Finally the present invention also relates to a new subtype 3a sequence as represented in SEQ ID NO 217 (see Figure 1).

Also included within the present invention are sequence variants of the polynucleic acids as selected from any of the nucleotide sequences as given in any of the above mentioned SEQ ID numbers, with said sequence variants containing either deletions and/or insertions of one or more nucleotides, mainly at the extremities of oligonucleotides (either 3' or 5'), or substitutions of some non-essential nucleotides by others (including modified nucleotides and/or inosine), for example, a type 1 or 2 sequence might be modified into a type 3 sequence by replacing some nucleotides of the type 1 or 2 sequence with type-specific nucleotides of type 3 as shown in Figure 1 (NS5 region), Figure 3 (Core region), Figure 4 (Core/E1 region), Figure 6 and 10 (NS3/NS4 region).

According to another embodiment, the present invention relates to a polynucleic acid composition as defined above, wherein said polynucleic acids correspond to a nucleotide sequence selected from any of the following HCV type 5 genomic sequences:

- an HCV genomic sequence as having a homology of more than 85%, preferably more than 86%, most preferably more than 87% homology to any of the sequences as represented in SEQ ID NO 41, 43, 45, 47, 49, 51, 53 (PC sequences) or 151 (BE95 sequence) in the region spanning positions 1 to 573 of the Core region as shown in Figure 9 and 3;
- an HCV genomic sequence as having a homology of more than 61%, preferably more than 63%, more preferably more than 65% homology, even more preferably more than 66% homology and most preferably more than 67% homology (f.i. 69 and 71%) to any of the sequences as represented in SEQ ID NO 41, 43, 45, 47, 49, 51, 53 (PC sequences), 153 or 155 (BE95, BE100 sequences) in the region spanning positions 574 to 957 of the E1 region as shown in Figure 4;
- an HCV genomic sequence having a homology of more than 76.5%, preferably of more than 77%, most preferably of more than 78% homology with any of the sequences as represented in SEQ ID NO 55, 57, 197 or 199 (PC sequences) in the region spanning positions 3856 to 4209 of the NS3 region as shown in Figure 6 or 10;
- an HCV genomic sequence having a homology of more than 68%, preferably of more than 70%, most preferably of more than 72% homology with the sequence as represented in SEQ ID NO 157 (BE95 sequence) in the region spanning positions 980 to 1179 of the E1/E2 region as shown in Figure 13;
- an HCV genomic sequence having a homology of more than 57%, preferably more than

59%, most preferably more than 61% homology to any of the sequences as represented in SEQ ID NO 59 or 61 (PC sequences) in the region spanning positions 4936 to 5296 of the NS4 region as shown in Figure 6 or 10;

- an HCV genomic sequence as having a homology of more than 93%, preferably more than 93.5%, most preferably more than 94% homology to any of the sequences as represented in SEQ ID NO 159 or 161 (BE95 or BE96 sequences) in the region spanning positions 7932 to 8271 of the NS5B region as shown in Figure 1.

Preferentially the above-mentioned genomic HCV sequences depict sequences from the coding regions of all the above-mentioned sequences.

According to the nucleotide distance classification system (with said nucleotide distances being calculated as explained above), said sequences of said composition are selected from:

- a nucleotide distance of less than 0.53, preferably less than 0.51, more preferably less than 0.49 for the E1 region to the type 5 sequences depicted above;
- a nucleotide distance of less than 0.3, preferably less than 0.28, more preferably of less than 0.26 for the Core region to the type 5 sequences depicted above;
- a nucleotide distance of less than 0.072, preferably less than 0.071, more preferably less than 0.070 for the NS5B region to the type 5 sequences as depicted above.

Isolates with similar sequences in the 5'UR to a group of isolates including SA1, SA3, and SA7 described in the 5'UR by Bukh et al. (1992), have been reported and described in the 5'UR and NS5 region as group V by Cha et al. (1992; WO 92/19743). This group of isolates belongs to type 5a as described in the present invention (SEQ ID NO 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 151, 153, 155, 157, 159, 161, 197 and 199).

Also included within the present invention are sequence variants of the polynucleic acids as selected from any of the nucleotide sequences as given in any of the above given SEQ ID numbers with said sequence variants containing either deletion and/or insertions of one or more nucleotides, mainly at the extremities of oligonucleotides (either 3' or 5'), or substitutions of some non-essential nucleotides (i.e. nucleotides not essential to discriminate between different genotypes of HCV) by others (including modified nucleotides an/or inosine), for example, a type 1 or 2 sequence might be modified into a type 5 sequence by replacing some nucleotides of the type 1 or 2 sequence with type-specific nucleotides of type 5 as shown in Figure 3 (Core region), Figure 4 (Core/E1 region), Figure 10 (NS3 / NS4 region), Figure 14 (E1/E2 region).

Another group of isolates including BU74 and BU79 having similar sequences in the 5'UR to isolates including Z6 and Z7 as described in the 5'UR by Bukh et al. (1992), have been described in the 5'UR and classified as a new type 4 by the inventors of this application (Stuyver et al., 1993). Coding sequences, including core, E1 and NS5 sequences of several new Gabonese isolates belonging to this group, are disclosed in the present invention (SEQ ID NO 106, 108, 110, 112, 114, 116, 118, 120 and 122).

According to yet another embodiment, the present invention relates to a composition as defined above, wherein said polynucleic acids correspond to a nucleotide sequence selected from any of the following HCV type 4 genomic sequences:

- an HCV genomic sequence having a homology of more than 66%, preferably more than 68%, most preferably more than 70% homology in the E1 region spanning positions 571 to 957 to any of the sequences as represented in SEQ ID NO 118, 120 or 122 (GB358, GB549, GB809 sequences) as shown in Figure 4;
- an HCV genomic sequence having a homology of more than 71%, preferably more than 72%, most preferably more than 74% homology to any of the sequences as represented in SEQ ID NO 118, 120 or 122 (GB358, GB549, GB809 sequences) in the region spanning positions 379 to 957 of the E1 region as shown in Figure 4;
- an HCV genomic sequence having a homology of more than 92%, preferably more than 93%, most preferably more than 94% homology to any of the sequences as represented in SEQ ID NO 163 or 165 (GB809, CAM600 sequences) in the region spanning positions 1 to 378 of the Core/E1 region as shown in Figure 4;
- an HCV genomic sequence (subtype 4c) having a homology of more than 85%, preferably more than 86%, more preferably more than 86.5% homology, most preferably more than 87, more than 88 or more than 89% homology to any of the sequences as represented in SEQ ID NO 183, 185 or 187 (GB116, GB215, GB809 sequences) in the region spanning positions 379 to 957 of the E1 region as shown in Figure 4;
- an HCV genomic sequence (subtype 4a) having a homology of more than 81%, preferably more than 83%, most preferably more than 85% homology to the sequence as represented in SEQ ID NO 189 (GB908 sequence) in the region spanning positions 379 to 957 of the E1 region as shown in Figure 4;
- an HCV genomic sequence (subtype 4e) having a homology of more than 85%, preferably more than 87%, most preferably more than 89% homology to any of the sequences as represented in SEQ ID NO 167 or 169 (CAM600, GB908 sequences) in the region

spanning positions 379 to 957 of the E1 region as shown in Figure 4;

- an HCV genomic sequence (subtype 4f) having a homology of more than 79%, preferably more than 81%, most preferably more than 83% homology to any of the sequences as represented in SEQ ID NO 171 or 173 (CAMG22, CAMG27 sequences) in the region spanning positions 379 to 957 of the E1 region as shown in Figure 4;
- an HCV genomic sequence (subtype 4g) having a homology of more than 84%, preferably more than 86%, most preferably more than 88% homology to the sequence as represented in SEQ ID NO 175 (GB549 sequence) in the region spanning positions 379 to 957 of the E1 region as shown in Figure 4;
- an HCV genomic sequence (subtype 4h) having a homology of more than 83%, preferably more than 85%, most preferably more than 87% homology to the sequence as represented in SEQ ID NO 177 (GB438 sequence) in the region spanning positions 379 to 957 of the E1 region as shown in Figure 4;
- an HCV genomic sequence (subtype 4i) as having a homology of more than 76%, preferably more than 78%, most preferably more than 80% homology to the sequence as represented in SEQ ID NO 179 (CAR4/1205 sequence) in the region spanning positions 379 to 957 of the E1 region as shown in Figure 4;
- an HCV genomic sequence (subtype 4j?) having a homology of more than 84%, preferably more than 86%, most preferably more than 88% homology to the sequence as represented in SEQ ID NO 181 (CAR4/901 sequence) in the region spanning positions 379 to 957 of the E1 region as shown in figure 4;
- an HCV genomic sequence as having a homology of more than 73%, preferably more than 75%, most preferably more than 77% homology to any of the sequences as represented in SEQ ID NO 106, 108, 110, 112, 114, or 116 (GB48, GB116, GB215, GB358, GB549, GB809 sequences) in the region spanning positions 7932 to 8271 of the NS5 region as shown in figure 1;
- an HCV genomic sequence (subtype 4c) having a homology of more than 88%, preferably more than 89%, most preferably more than 90% homology to any of the sequences as represented in SEQ ID NO 106, 108, 110, or 112 (GB48, GB116, GB215, GB358 sequences) in the region spanning positions 7932 to 8271 of the NS5 region as shown in Figure 1;
- an HCV genomic sequence (subtype 4e) having a homology of more than 88%, preferably more than 89%, most preferably more than 90% homology to any of the sequences as

represented in SEQ ID NO 116 or 201 (GB809 or CAM 600 sequences) in the region spanning positions 7932 to 8271 of the NS5 region as shown in Figure 1;

- an HCV genomic sequence (subtype 4f) having a homology of more than 87%, preferably more than 89%, most preferably more than 90% homology to the sequence as represented in SEQ ID NO 203 (CAMG22 sequence) in the region spanning positions 7932 to 8271 of the NS5 region as shown in Figure 1;
- an HCV genomic sequence (subtype 4g) as having a homology of more than 85%, preferably more than 87%, most preferably more than 89% homology to the sequence as represented in SEQ ID NO 114 (GB549 sequence) in the region spanning positions 7932 to 8271 of the NS5 region as shown in Figure 1;
- an HCV genomic sequence (subtype 4h) as having a homology of more than 86%, preferably more than 87%, more preferably more than 88% homology, more preferably more than 89% homology to the sequence as represented in SEQ ID NO 207 (GB437 sequence) in the region spanning positions 7932 to 8271 of the NS5 region as shown in Figure 1;
- an HCV genomic sequence (subtype 4i) having a homology of more than 84%, preferably more than 86%, most preferably more than 88% homology to the sequence as represented in SEQ ID NO 209 (CAR4/1205 sequence) in the region spanning positions 7932 to 8271 of the NS5 region as shown in figure 1;
- an HCV genomic sequence (subtype 4j) having a homology of more than 81%, preferably more than 83%, most preferably more than 85% homology to the sequence as represented in SEQ ID NO 211 (CAR1/501 sequence) in the region spanning positions 7932 to 8271 of the NS5 region as shown in figure 1.

Preferentially the above-mentioned genomic HCV sequences depict sequences from the coding regions of all the above-mentioned sequences.

According to the nucleotide distance classification system (with said nucleotide distances being calculated as explained above), said sequences of said composition are selected from:

- an HCV genomic sequence (type 4) being characterized as having a nucleotide distance of less than 0.52, 0.50, 0.4880, 0.46, 0.44, 0.43 or most preferably less than 0.42 in the region spanning positions 574 to 957 to any of the sequences as represented in SEQ ID NO 118, 120 or 122 in the region spanning positions 1 to 957 of the Core/E1 region as shown in Figure 4;
- an HCV genomic sequence (type 4) being characterized as having a nucleotide distance of

less than 0.39, 0.36, 0.34, 0.32 or most preferably less than 0.31 to any of the sequences as represented in SEQ ID NO 118, 120 or 122 in the region spanning positions 379 to 957 of the E1 region as shown in Figure 4;

- an HCV genomic sequence (subtype 4c) being characterized as having a nucleotide distance of less than 0.27, 0.26, 0.24, 0.22, 0.20, 0.18, 0.17, 0.162, 0.16 or most preferably less than 0.15 to any of the sequences as represented in SEQ ID NO 183, 185 or 187 in the region spanning positions 379 to 957 of the E1 region as shown in Figure 4;
- an HCV genomic sequence (subtype 4a) being characterized as having a nucleotide distance of less than 0.30, 0.28, 0.26, 0.24, 0.22, 0.21 or most preferably of less than 0.205 to the sequence as represented in SEQ ID NO 189 in the region spanning positions 379 to 957 of the E1 region as shown in Figure 4;
- an HCV genomic sequence (subtype 4e) being characterized as having a nucleotide distance of less than 0.26, 0.25, 0.23, 0.21, 0.19, 0.17, 0.165, most preferably less than 0.16 to any of the sequences as represented in SEQ ID NO 167 or 169 in the region spanning positions 379 to 957 of the E1 region as shown in Figure 4;
- an HCV genomic sequence (subtype 4f) being characterized as having a nucleotide distance of less than 0.26, 0.24, 0.22, 0.20, 0.18, 0.16, 0.15 or most preferably less than 0.14 to any of the sequences as represented in SEQ ID NO 171 or 173 in the region spanning positions 379 to 957 of the E1 region as shown in Figure 4;
- an HCV genomic sequence (subtype 4g) being characterized as having a nucleotide distance of less than 0.20, 0.19, 0.18, 0.17 or most preferably of less than 0.16 to the sequence as represented in SEQ ID NO 175 in the region spanning positions 379 to 957 of the E1 region as shown in Figure 4;
- an HCV genomic sequence (subtype 4h) being characterized as having a nucleotide distance of less than 0.20, 0.19, 0.18, 0.17 and most preferably of less than 0.16 to the sequence as represented in SEQ ID NO 177 in the region spanning positions 379 to 957 of the E1 region as shown in Figure 4;
- an HCV genomic sequence (subtype 4i) being characterized as having a nucleotide distance of less than 0.27, 0.25, 0.23, 0.21 and preferably less than 0.16 to the sequence as represented in SEQ ID NO 179 in the region spanning positions 379 to 957 of the E1 region as shown in Figure 4;
- an HCV genomic sequence (subtype 4j?) being characterized as having a nucleotide distance of less than 0.19, 0.18, 0.17, 0.165 and most preferably of less than 0.16 to the

sequence as represented in SEQ ID NO 181 in the region spanning positions 379 to 957 of the E1 region as shown in figure 4;

- an HCV genomic sequence (type 4) being characterized as having a nucleotide distance of less than 0.35, 0.34, 0.32 and most preferably of less than 0.30 to any of the sequences as represented in SEQ ID NO 106, 108, 110, 112, 114, or 116 in the region spanning positions 7932 to 8271 of the NS5 region as shown in figure 1;
- an HCV genomic sequence (subtype 4c) being characterized as having a nucleotide distance of less than 0.18, 0.16, 0.14, 0.135, 0.13, 0.1275 or most preferably less than 0.125 to any of the sequences as represented in SEQ ID NO 106, 108, 110, or 112 in the region spanning positions 7932 to 8271 of the NS5 region as shown in Figure 1;
- an HCV genomic sequence (subtype 4e) being characterized as having a nucleotide distance of less than 0.15, 0.14, 0.135, 0.13 and most preferably of less than 0.125 to any of the sequences as represented in SEQ ID NO 116 or 201 in the region spanning positions 7932 to 8271 of the NS5 region as shown in Figure 1;
- an HCV genomic sequence (subtype 4f) being characterized as having a nucleotide distance of less than 0.15, 0.14, 0.135, 0.13 or most preferably less than 0.125 to the sequence as represented in SEQ ID NO 203 in the region spanning positions 7932 to 8271 of the NS5 region as shown in Figure 1;
- an HCV genomic sequence (subtype 4g) being characterized as having a nucleotide distance of less than 0.17, 0.16, 0.15, 0.14, 0.13 or most preferably less than 0.125 to the sequence as represented in SEQ ID NO 114 in the region spanning positions 7932 to 8271 of the NS5 region as shown in Figure 1;
- an HCV genomic sequence (subtype 4h) being characterized as having a nucleotide distance of less than 0.155, 0.15, 0.145, 0.14, 0.135, 0.13 or most preferably less than 0.125 to the sequence as represented in SEQ ID NO 207 in the region spanning positions 7932 to 8271 of the NS5 region as shown in Figure 1;
- an HCV genomic sequence (subtype 4i) being characterized as having a nucleotide distance of less than 0.17, 0.16, 0.15, 0.14, 0.13 or most preferably of less than 0.125 to the sequence as represented in SEQ ID NO 209 in the region spanning positions 7932 to 8271 of the NS5 region as shown in figure 1;
- an HCV genomic sequence (subtype 4j) being characterized as having a nucleotide distance of less than 0.21, 0.20, 0.19, 0.18, 0.17, 0.16, 0.15, 0.14, 0.13 and most preferably of less than 0.125 to the sequence as represented in SEQ ID NO 211 in the region spanning

positions 7932 to 8271 of the NS5 region as shown in figure 1.

Also included within the present invention are sequence variants of the polynucleic acids as selected from any of the nucleotide sequences as given in any of the above given SEQ ID numbers with said sequence variants containing either deletion and/or insertions of one or more nucleotides, mainly at the extremities of oligonucleotides (either 3' or 5'), or substitutions of some non-essential nucleotides (i.e. nucleotides not essential to discriminate between different genotypes of HCV) by others (including modified nucleotides an/or inosine), for example, a type 1 or 2 sequence might be modified into a type 4 sequence by replacing some nucleotides of the type 1 or 2 sequence with type-specific nucleotides of type 4 as shown in Figure 3 (Core region), Figure 4 (Core/E1 region), Figure 10 (NS3 / NS4 region), Figure 14 (E1/E2 region).

The present invention also relates to a sequence as represented in SEQ ID NO 193 (GB724 sequence).

After aligning NS5 or E1 sequences of GB48, GB, 116, GB215, GB358, GB549 and GB809, these isolates clearly segregated into 3 subtypes within type 4 : GB48, GB116, GB215 and GB358 belong to the subtype designated 4c, GB549 to subtype 4g and GB809 to subtype 4e. In NS5, GB809 (subtype 4e) showed a higher nucleic acids homology to subtype 4c isolates (85.6 - 86.8%) than to GB549 (subtype 4g, 79.7%), while GB549 showed similar homologies to both other subtypes (78.8 to 80% to subtype 4c and 79.7% to subtype 4e). In E1, subtype 4c showed equal nucleic acid homologies of 75.2% to subtypes 4g and 4e while 4g and 4e were 78.4% homologous. At the amino acid level however, subtype 4e showed a normal homology to subtype 4c (80.2%), while subtype 4g was more homologous to 4c (83.3%) and 4e (84.1%).

According to yet another embodiment, the present invention relates to a composition as defined above, wherein said polynucleic acids correspond to a nucleotide sequence selected from any of the following HCV type 2d genomic sequences:

- an HCV genomic sequence as having a homology of more than 78%, preferably more than 80%, most preferably more than 82% homology to the sequence as represented in SEQ ID NO (NE92) 143 in the region spanning positions 379 to 957 of the Core/E1 region as shown in Figure 4;
- an HCV genomic sequence as having a homology of more than 74%, preferably more than 76%, most preferably more than 78% homology to the sequence as represented in SEQ ID NO 143 (NE92) in the region spanning positions 574 to 957 as shown in Figure 4;

- an HCV genomic sequence as having a homology of more than 87%, preferably more than 89%, most preferably more than 91% homology to the sequence as represented in SEQ ID NO 145 (NE92) in the region spanning positions 7932 to 8271 of the NS5B region as shown in Figure 1.

Preferentially the above-mentioned genomic HCV sequences depict sequences from the coding regions of all the above-mentioned sequences.

According to the nucleotide distance classification system (with said nucleotide distances being calculated as explained above), said sequences of said composition are selected from:

- a nucleotide distance of less than 0.32, preferably less than 0.31, more preferably less than 0.30 for the E1 region (574 to 957) to any of the above specified sequences;
- a nucleotide distance of less than 0.08, preferably less than 0.07, more preferably less than 0.06 for the Core region (1 to 378) to any of the above given sequences
- a nucleotide distance of less than 0.15, preferentially less than 0.13, more preferentially less than 0.12 for the NS5B region to any of the above-specified sequences.

Polynucleic acid sequences according to the present invention which are homologous to the sequences as represented by a SEQ ID NO can be characterized and isolated according to any of the techniques known in the art, such as amplification by means of type or subtype specific primers, hybridization with type or subtype specific probes under more or less stringent conditions, serological screening methods (see examples 4 and 11) or via the LiPA typing system.

Polynucleic acid sequences of the genomes indicated above from regions not yet depicted in the present examples, figures and sequence listing can be obtained by any of the techniques known in the art, such as amplification techniques using suitable primers from the type or subtype specific sequences of the present invention.

The present invention relates also to a composition as defined above, wherein said polynucleic acid is liable to act as a primer for amplifying the nucleic acid of a certain isolate belonging to the genotype from which the primer is derived.

An example of a primer according to this embodiment of the invention is HCPr 152 as shown in table 7 (SEQ ID NO 79).

The term "primer" refers to a single stranded DNA oligonucleotide sequence capable of acting as a point of initiation for synthesis of a primer extension product which is complementary to the nucleic acid strand to be copied. The length and the sequence of the primer must be such that they allow to prime the synthesis of the extension products.

Preferably the primer is about 5-50 nucleotides. Specific length and sequence will depend on the complexity of the required DNA or RNA targets, as well as on the conditions of primer use such as temperature and ionic strength.

The fact that amplification primers do not have to match exactly with corresponding template sequence to warrant proper amplification is amply documented in the literature (Kwok et al., 1990).

The amplification method used can be either polymerase chain reaction (PCR; Saiki et al., 1988), ligase chain reaction (LCR; Landgren et al., 1988; Wu & Wallace, 1989; Barany, 1991), nucleic acid sequence-based amplification (NASBA; Guatelli et al., 1990; Compton, 1991), transcription-based amplification system (TAS; Kwok et al., 1989), strand displacement amplification (SDA; Duck, 1990; Walker et al., 1992) or amplification by means of Q β replicase (Lizardi et al., 1988; Lomeli et al., 1989) or any other suitable method to amplify nucleic acid molecules using primer extension. During amplification, the amplified products can be conveniently labelled either using labelled primers or by incorporating labelled nucleotides. Labels may be isotopic (32 P, 35 S, etc.) or non-isotopic (biotin, digoxigenin, etc.). The amplification reaction is repeated between 20 and 80 times, advantageously between 30 and 50 times.

The present invention also relates to a composition as defined above, wherein said polynucleic acid is able to act as a hybridization probe for specific detection and/or classification into types of a nucleic acid containing said nucleotide sequence, with said oligonucleotide being possibly labelled or attached to a solid substrate.

The term "probe" refers to single stranded sequence-specific oligonucleotides which have a sequence which is complementary to the target sequence of the HCV genotype(s) to be detected.

Preferably, these probes are about 5 to 50 nucleotides long, more preferably from about 10 to 25 nucleotides.

The term "solid support" can refer to any substrate to which an oligonucleotide probe can be coupled, provided that it retains its hybridization characteristics and provided that the background level of hybridization remains low. Usually the solid substrate will be a microtiter plate, a membrane (e.g. nylon or nitrocellulose) or a microsphere (bead). Prior to application to the membrane or fixation it may be convenient to modify the nucleic acid probe in order to facilitate fixation or improve the hybridization efficiency. Such modifications may encompass homopolymer tailing, coupling with different reactive groups such as aliphatic

groups, NH₂ groups, SH groups, carboxylic groups, or coupling with biotin or haptens.

The present invention also relates to the use of a composition as defined above for detecting the presence of one or more HCV genotypes, more particularly for detecting the presence of a nucleic acid of any of the HCV genotypes having a nucleotide sequence as defined above, present in a biological sample liable to contain them, comprising at least the following steps:

- (i) possibly extracting sample nucleic acid,
- (ii) possibly amplifying the nucleic acid with at least one of the primers as defined above or any other HCV subtype 2d, HCV type 3, HCV type 4, HCV type 5 or universal HCV primer,
- (iii) hybridizing the nucleic acids of the biological sample, possibly under denatured conditions, and with said nucleic acids being possibly labelled during or after amplification, at appropriate conditions with one or more probes as defined above, with said probes being preferably attached to a solid substrate,
- (iv) washing at appropriate conditions,
- (v) detecting the hybrids formed,
- (vi) inferring the presence of one or more HCV genotypes present from the observed hybridization pattern.

Preferably, this technique could be performed in the Core or NS5B region.

The term "nucleic acid" can also be referred to as analyte strand and corresponds to a single- or double-stranded nucleic acid molecule. This analyte strand is preferentially positive- or negative stranded RNA, cDNA or amplified cDNA.

The term "biological sample" refers to any biological sample (tissue or fluid) containing HCV nucleic acid sequences and refers more particularly to blood serum or plasma samples.

The term "HCV subtype 2d primer" refers to a primer which specifically amplifies HCV subtype 2d sequences present in a sample (see Examples section and figures).

The term "HCV type 3 primer" refers to a primer which specifically amplifies HCV type 3 sequences present in a sample (see Examples section and figures).

The term "HCV type 4 primer" refers to a primer which specifically amplifies HCV type 4 genomes present in a sample.

The term "universal HCV primer" refers to oligonucleotide sequences complementary to any of the conserved regions of the HCV genome.

The term "HCV type 5 primer" refers to a primer which specifically amplifies HCV type

5 genomes present in a sample. The term "universal HCV primer" refers to oligonucleotide sequences complementary to any of the conserved regions of the HCV genome.

The expression "appropriate" hybridization and washing conditions are to be understood as stringent and are generally known in the art (e.g. Maniatis et al., Molecular Cloning: A Laboratory Manual, New York, Cold Spring Harbor Laboratory, 1982).

However, according to the hybridization solution (SSC, SSPE, etc.), these probes should be hybridized at their appropriate temperature in order to attain sufficient specificity.

The term "labelled" refers to the use of labelled nucleic acids. This may include the use of labelled nucleotides incorporated during the polymerase step of the amplification such as illustrated by Saiki et al. (1988) or Bej et al. (1990) or labelled primers, or by any other method known to the person skilled in the art.

The process of the invention comprises the steps of contacting any of the probes as defined above, with one of the following elements:

- either a biological sample in which the nucleic acids are made available for hybridization,
- or the purified nucleic acids contained in the biological sample
- or a single copy derived from the purified nucleic acids,
- or an amplified copy derived from the purified nucleic acids, with said elements or with said probes being attached to a solid substrate.

The expression "inferring the presence of one or more HCV genotypes present from the observed hybridization pattern" refers to the identification of the presence of HCV genomes in the sample by analyzing the pattern of binding of a panel of oligonucleotide probes. Single probes may provide useful information concerning the presence or absence of HCV genomes in a sample. On the other hand, the variation of the HCV genomes is dispersed in nature, so rarely is any one probe able to identify uniquely a specific HCV genome. Rather, the identity of an HCV genotype may be inferred from the pattern of binding of a panel of oligonucleotide probes, which are specific for (different) segments of the different HCV genomes. Depending on the choice of these oligonucleotide probes, each known HCV genotype will correspond to a specific hybridization pattern upon use of a specific combination of probes. Each HCV genotype will also be able to be discriminated from any other HCV genotype amplified with the same primers depending on the choice of the oligonucleotide probes. Comparison of the generated pattern of positively hybridizing probes for a sample containing one or more unknown HCV sequences to a scheme of expected

hybridization patterns, allows one to clearly infer the HCV genotypes present in said sample.

The present invention thus relates to a method as defined above, wherein one or more hybridization probes are selected from any of SEQ ID NO 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59 or 61, 106, 108, 110, 112, 114, 116, 118, 120, 122, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 198, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 222, 269 or sequence variants thereof, with said sequence variants containing deletions and/or insertions of one or more nucleotides, mainly at their extremities (either 3' or 5'), or substitutions of some non-essential nucleotides (i.e. nucleotides not essential to discriminate between genotypes) by others (including modified nucleotides or inosine), or with said variants consisting of the complement of any of the above-mentioned oligonucleotide probes, or with said variants consisting of ribonucleotides instead of deoxyribonucleotides, all provided that said variant probes can be caused to hybridize with the same specificity as the oligonucleotide probes from which they are derived.

In order to distinguish the amplified HCV genomes from each other, the target polynucleic acids are hybridized to a set of sequence-specific DNA probes targetting HCV genotypic regions located in the HCV polynucleic acids.

Most of these probes target the most type-specific regions of HCV genotypes, but some can be caused to hybridize to more than one HCV genotype.

According to the hybridization solution (SSC, SSPE, etc.), these probes should be stringently hybridized at their appropriate temperature in order to attain sufficient specificity. However, by slightly modifying the DNA probes, either by adding or deleting one or a few nucleotides at their extremities (either 3' or 5'), or substituting some non-essential nucleotides (i.e. nucleotides not essential to discriminate between types) by others (including modified nucleotides or inosine) these probes or variants thereof can be caused to hybridize specifically at the same hybridization conditions (i.e. the same temperature and the same hybridization solution). Also changing the amount (concentration) of probe used may be beneficial to obtain more specific hybridization results. It should be noted in this context, that probes of the same length, regardless of their GC content, will hybridize specifically at approximately the same temperature in TMACl solutions (Jacobs et al., 1988).

Suitable assay methods for purposes of the present invention to detect hybrids formed between the oligonucleotide probes and the nucleic acid sequences in a sample may comprise

any of the assay formats known in the art, such as the conventional dot-blot format, sandwich hybridization or reverse hybridization. For example, the detection can be accomplished using a dot blot format, the unlabelled amplified sample being bound to a membrane, the membrane being incorporated with at least one labelled probe under suitable hybridization and wash conditions, and the presence of bound probe being monitored.

An alternative and preferred method is a "reverse" dot-blot format, in which the amplified sequence contains a label. In this format, the unlabelled oligonucleotide probes are bound to a solid support and exposed to the labelled sample under appropriate stringent hybridization and subsequent washing conditions. It is to be understood that also any other assay method which relies on the formation of a hybrid between the nucleic acids of the sample and the oligonucleotide probes according to the present invention may be used.

According to an advantageous embodiment, the process of detecting one or more HCV genotypes contained in a biological sample comprises the steps of contacting amplified HCV nucleic acid copies derived from the biological sample, with oligonucleotide probes which have been immobilized as parallel lines on a solid support.

According to this advantageous method, the probes are immobilized in a Line Probe Assay (LiPA) format. This is a reverse hybridization format (Saiki et al., 1989) using membrane strips onto which several oligonucleotide probes (including negative or positive control oligonucleotides) can be conveniently applied as parallel lines.

The invention thus also relates to a solid support, preferably a membrane strip, carrying on its surface, one or more probes as defined above, coupled to the support in the form of parallel lines.

The LiPA is a very rapid and user-friendly hybridization test. Results can be read 4 h. after the start of the amplification. After amplification during which usually a non-isotopic label is incorporated in the amplified product, and alkaline denaturation, the amplified product is contacted with the probes on the membrane and the hybridization is carried out for about 1 to 1,5 h hybridized polynucleic acid is detected. From the hybridization pattern generated, the HCV type can be deduced either visually, but preferably using dedicated software. The LiPA format is completely compatible with commercially available scanning devices, thus rendering automatic interpretation of the results very reliable. All those advantages make the LiPA format liable for the use of HCV detection in a routine setting. The LiPA format should be particularly advantageous for detecting the presence of different HCV genotypes.

The present invention also relates to a method for detecting and identifying novel HCV

genotypes, different from the known HCV genomes, comprising the steps of:

- determining to which HCV genotype the nucleotides present in a biological sample belong, according to the process as defined above,
- in the case of observing a sample which does not generate a hybridization pattern compatible with those defined in Table 3, sequencing the portion of the HCV genome sequence corresponding to the aberrantly hybridizing probe of the new HCV genotype to be determined.

The present invention also relates to the use of a composition as defined above, for detecting one or more genotypes of HCV present in a biological sample liable to contain them, comprising the steps of:

- (i) possibly extracting sample nucleic acid,
- (ii) amplifying the nucleic acid with at least one of the primers as defined above,
- (iii) sequencing the amplified products
- (iv) inferring the HCV genotypes present from the determined sequences by comparison to all known HCV sequences.

The present invention also relates to a composition consisting of or comprising at least one peptide or polypeptide comprising a contiguous sequence of at least 5 amino acids corresponding to a contiguous amino acid sequence encoded by at least one of the HCV genomic sequences as defined above, having at least one amino acid differing from the corresponding region of known HCV (type 1 and/or type 2 and/or type 3) polyprotein sequences as shown in Table 3, or muteins thereof.

It is to be noted that, at the level of the amino acid sequence, an amino acid difference (with respect to known HCV amino acid sequences) is necessary, which means that the polypeptides of the invention correspond to polynucleic acids having a nucleotide difference (with known HCV polynucleic acid sequences) involving an amino acid difference.

The new amino acid sequences, as deduced from the disclosed nucleotide sequences (see SEQ ID NO 1 to 62 and 106 to 123 and 143 to 218, 223 and 270), show homologies of only 59.9 to 78% with prototype sequences of type 1 and 2 for the NS4 region, and of only 53.9 to 68.8% with prototype sequences of type 1 and 2 for the E1 region. As the NS4 region is known to contain several epitopes, for example characterized in patent application EP-A-0 489 968, and as the E1 protein is expected to be subject to immune attack as part of the viral envelope and expected to contain epitopes, the NS4 and E1 epitopes of the new type 3, 4 and 5 isolates will consistently differ from the epitopes present in type 1 and 2 isolates. This is

examplified by the type-specificity of NS4 synthetic peptides as presented in example 4, and the type-specificity of recombinant E1 proteins in example 11.

After aligning the new subtype 2d, type 3, 4 and 5 (see SEQ ID NO 1 to 62 and 106 to 123 and 143 to 218, 223 and 270) amino acid sequences with the prototype sequences of type 1a, 1b, 2a, and 2b, type- and subtype-specific variable regions can be delineated as presented in Figure 5 and 7.

As to the muteins derived from the polypeptides of the invention, Table 4 gives an overview of the amino acid substitutions which could be the basis of some of the muteins as defined above.

The peptides according to the present invention contain preferably at least 5 contiguous HCV amino acids, preferably however at least 8 contiguous amino acids, at least 10 or at least 15 (for instance at least 9, 11, 12, 13, 14, 20 or 25 amino acids) of the new HCV sequences of the invention.

TABLE 4

Amino acids	Synonymous groups
Ser (S)	Ser, Thr, Gly, Asn
Arg (R)	Arg, His, Lys, Glu, Gln
Leu (L)	Leu; Ile, Met, Phe, Val, Tyr
Pro (P)	Pro, Ala, Thr, Gly
Thr (T)	Thr, Pro, Ser, Ala, Gly, His, Gln
Ala (A)	Ala, Pro, Gly, Thr
Val (V)	Val, Met, Ile, Tyr, Phe, Leu, Val
Gly (G)	Gly, Ala, Thr, Pro, Ser
Ile (I)	Ile, Met, Leu, Phe, Val, Ile, Tyr
Phe (F)	Phe, Met, Tyr, Ile, Leu, Trp, Val
Tyr (Y)	Tyr, Phe, Trp, Met, Ile, Val, Leu
Cys (C)	Cys, Ser, Thr, Met
His (H)	His, Gln, Arg, Lys, Glu, Thr
Gln (Q)	Gln, Glu, His, Lys, Asn, Thr, Arg
Asn (N)	Asn, Asp, Ser, Gln
Lys (K)	Lys, Arg, Glu, Gln, His
Asp (D)	Asp, Asn, Glu, Gln
Glu (E)	Glu, Gln, Asp, Lys, Asn, His, Arg
Met (M)	Met, Ile, Leu, Phe, Val

The polypeptides of the invention, and particularly the fragments, can be prepared by classical chemical synthesis.

The synthesis can be carried out in homogeneous solution or in solid phase.

For instance, the synthesis technique in homogeneous solution which can be used is the one described by Houbenweyl in the book entitled "Methode der organischen chemie" (Method of organic chemistry) edited by E. Wunsh, vol. 15-I et II. THIEME, Stuttgart 1974.

The polypeptides of the invention can also be prepared in solid phase according to the methods described by Atherton and Shepard in their book entitled "Solid phase peptide synthesis" (IRL Press, Oxford, 1989).

The polypeptides according to this invention can be prepared by means of recombinant DNA techniques as described by Maniatis et al., Molecular Cloning: A Laboratory Manual, New York, Cold Spring Harbor Laboratory, 1982).

The present invention relates particularly to a polypeptide or peptide composition as defined above, wherein said contiguous sequence contains in its sequence at least one of the following amino acid residues:

L7, Q43, M44, S60, R67, Q70, T71, A79, A87, N106, K115, A127, A190, S130, V134, G142, I144, E152, A157, V158, P165, S177 or Y177, I178, V180 or E180 or F182, R184, I186, H187, T189, A190, S191 or G191, Q192 or L192 or I192 or V192 or E192, N193 or H193 or P193, W194 or Y194, H195, A197 or I197 or V197 or T197, V202, I203 or L203, Q208, A210, V212, F214, T216, R217 or D217 or E217 or V217, H218 or N218, H219 or V219 or L219, L227 or I227, M231 or E231 or Q231, T232 or D232 or A232 or K232, Q235 or I235, A237 or T237, I242, I246, S247, S248, V249, S250 or Y250, I251 or V251 or M251 or F251, D252, T254 or V254, L255 or V255, E256 or A256, M258 or F258 or V258, A260 or Q260 or S260, A261, T264 or Y264, M265, I266 or A266, A267, G268 or T268, F271 or M271 or V271, I277, M280 or H280, I284 or A284 or L84, V274, V291, N292 or S292, R293 or I293 or Y293, Q294 or R294, L297 or I297 or Q297, A299 or K299 or Q299, N303 or T303, T308 or L308, T310 or F310 or A310 or D310 or V310, L313, G317 or Q317, L333, S351, A358, A359, A363, S364, A366, T369, L373, F376, Q386, I387, S392, I399, F402, I403, R405, D454, A461, A463, T464, K484, Q500, E501, S521, K522, H524, N528, S531, S532, V534, F536, F537, M539, I546, C1282, A1283, H1310, V1312, Q1321, P1368, V1372, V1373, K1405, Q1406, S1409, A1424, A1429, C1435, S1436, S1456, H1496, A1504, D1510, D1529, I1543, N1567, D1556, N1567, M1572, Q1579, L1581, S1583, F1585, V1595, E1606 or T1606, M1611, V1612 or L1612, P1630, C1636, P1651, T1656 or I1656, L1663, V1667, V1677, A1681, H1685, E1687, G1689, V1695, A1700, Q1704, Y1705, A1713, A1714 or S1714, M1718, D1719, A1721 or T1721, R1722, A1723 or V1723, H1726 or G1726, E1730, V1732, F1735, I1736, S1737, R1738, T1739, G1740, Q1741, K1742, Q1743, A1744, T1745, L1746, E1747 or K1747, I1749, A1750, T1751 or A1751, V1753, N1755, K1756, A1757, P1758, A1759, H1762, T1763, Y1764, P2645, A2647, K2650, K2653 or L2653, S2664, N2673, F2680, K2681, L2686, H2692, Q2695 or L2695 or I2695, V2712, F2715, V2719 or Q2719, T2722, T2724, S2725, R2726, G2729, Y2735, H2739, I2748, G2746 or I2746, I2748, P2752 or K2752, P2754 or T2754, T2757 or P2757,

with said notation being composed of a letter representing the amino acid residue by its one-letter code, and a number representing the amino acid numbering according to Kato et al., 1990 as shown in Table 1 (comparison with other isolates). See also the numbering in Figures 2, 5, 7, and 11 (alignment amino acid sequences).

Within the group of unique and new amino acid residues of the present invention, the following residues were found to be specific for the following types of HCV according to the

HCV classification system used in the present invention:

- Q208, R217, E231, I235, I246, T264, I266, A267, F271, K299, L2686, Q2719 which are specific for the HCV subtype 2d sequences of the present invention as shown in Fig. 5 and 2;
- Q43, S60, R67, F182, I186, H187, A190, S191, L192, W194, V202, L203, V219, Q231, D232, A237, T254, M280, Q299, T303, L308, and/or L313 which are specific for the Core/E1 region of HCV type 3 of the invention as shown in Fig. 5;
- D1556, Q1579, L1581, S1584, F1585, E1606, V1612, P1630, C1636, T1656, L1663, H1685, E1687, G1689, V1695, Y1705, A1713, A1714, A1721, V1723, H1726, R1738, Q1743, A1744, E1747, I1749, A1751, A1759 and/or H1762 which are specific for the NS3/4 region of HCV type 3 sequences of the invention as shown in Fig. 7;
- K2665, D2666, R2670 which are specific for the NS5B region of HCV type 3 of the invention as shown in Fig. 2;
- L7, A79, A127, S130, E152, V158, S177 or Y177, V180 or E180, R184, T189, Q192 or E192 or I192, N193 or H193, I197 or V197, I203, A210, V212, E217, H218, H219, L227, A232, V249, I251 or M251, D252, L255 or V255, E256, M258 or V258 or F258, A260 or Q260, M265, T268, V271, V274, M280, I284, N292 or S292, Q294, L297 or I297, T308, A310 or D310 or V310 or T310, and G317 which are specific for the core/E1 region of HCV type 4 sequences of the present invention as shown in Fig. 5;
- P2645, K2650, K2653, G2656, V2658, T2668, N2673 or N2673, K2681, H2686, D2691, L2692, Q2695 or L2695 or I2695, Y2704, V2712, F2715, V2719, I2722, S2725, G2729, Y2735, G2746 or I2746, P2752 or K2752, Q2753, P2754 or T2754, T2757 or P2757 which are specific for the NS5B region of the HCV type 4 sequences of the present invention as shown in Fig. 2;
- M44, Q70, A87, N106, K115, V137, G142, P165, I178, F251, A299, N303, Q317 which are specific for the Core/E1 region of the HCV type 4 sequences of the present invention as shown in Fig. 5;
- L333, S351, A358, A359, A363, S364, A366, T369, L373, F376, Q386, I387, S392, I399, F102, I403, R405, D454, A461, A463, T464, K484, Q500, E501, S521, K522, H524, N528, S532, V534, F537, M539, I546 which are specific for

the E1/E2 region of the HCV type 5 sequences of the present invention as shown in Fig. 12;

- C1282, A1283, V1312, Q1321, P1368, V1372, K1405, Q1406, S1409, A1424, A1429, C1435, S1436, S1456, H1496, A1504, D1510, D1529, I1543, N1567, M1572, V1595, T1606, M1611, L1612, I1656, V1667, A1681, A1700, A1713, S1714, M1718, D1719, T1721, R1722, A1723, G1726, F1735, I1736, S1737, T1739, G1740, K1742, T1745, L1746, K1747, A1750, V1753, N1755, A1757, D1758, T1763, and Y1764 which are specific for the NS3/NS4 region of HCV type 5 sequences of the invention as shown in Fig. 7;
- A2647, L2653, S2674, F2680, T2724, R2726, Y2730, H2739 which are specific for the NS5B region of the HCV type 5 sequences of the present invention as shown in Fig. 2;
- A256, P1631, V1677, Q1704, E1730, V1732, Q1741 and T1751 which are specific for the HCV type 3 and 5 sequences of the present invention as shown in Fig. 5 and 7;
- T71, A157, I227, T237, T240, Y250, V251, S260, M271, T2673, T2722, I2748 which are specific for the HCV type 3 and 4 sequences of the present invention as shown in Fig. 5 and 2,
- V192, Y194, A197, P249, S250, R294 which are specific for the HCV type 4 and 5 sequences of the present invention as shown in Fig. 5;
- I293 which is specific for the HCV type 4 and subtype 2d sequence of the present invention as shown in Fig. 5;
- D217 and R294 which are specific for the HCV type 3, 4 and 5 sequences of the present invention as shown in Fig. 5;
- L192 which is specific for the HCV type 3 and subtype 2d sequences of the present invention as shown in Fig. 5;
- G191 and T197 which are specific for the HCV type 3, 4 and subtype 2d sequences of the present invention as shown in Fig. 5;
- K232 which is specific for the HCV subtype 2d en type 5 sequences of the present invention as shown in Fig. 5.

and with said notation being composed of a letter, unambiguously representing the amino acid by its one-letter code, and a number representing the amino acid numbering according to Kato et al., 1990 (see also Table 1 for comparison with other isolates), as well as Figure 2 (NS5

region), Figure 5 (Core/E1 region), Figure 7 (NS3/NS4 region), Figure 12 (E1/E2 region). Some of the above-mentioned amino acids may be contained in type or subtype specific epitopes.

For example M231 (detected in type 5) refers to a methionine at position 231. A glutamine (Q) is present at the same position 231 in type 3 isolates, whereas this position is occupied by an arginine in type 1 isolates and by a lysine (K) or asparagine (N) in type 2 isolates (see Figure 5).

The peptide or polypeptide according to this embodiment of the invention may be possibly labelled, or attached to a solid substrate, or coupled to a carrier molecule such as biotin, or mixed with a proper adjuvant.

The variable region in the core protein (V-CORE in Fig. 5) has been shown to be useful for serotyping (Machida et al., 1992). The sequence of the disclosed type 5 sequence in this region shows type-specific features. The peptide from amino acid 70 to 78 shows the following unique sequence for the sequences of the present invention (see figure 5):

QPTGRSWGQ (SEQ ID NO 93)

RSEGRTSWAQ (SEQ ID NO 220)

and RTEGRTSWAQ (SEQ ID NO 221)

Another preferred V-Core spanning region is the peptide spanning positions 60 to 78 of subtype 3c with sequence:

SRRQPIPRARRTEGRSWAQ (SEQ ID NO 268)

Five type-specific variable regions (V1 to V5) can be identified after aligning E1 amino acid sequences of the 4 genotypes, as shown in Figure 5.

Region V1 encompasses amino acids 192 to 203, this is the amino-terminal 10 amino acids of the E1 protein. The following unique sequences as shown in Fig. 5 can be deduced:

LEWRNTSGLYVL (SEQ ID NO 83)

VNYRNASGIYHI (SEQ ID NO 126)

QHYRNISGIYHV (SEQ ID NO 127)

EHYRNASGIYHI (SEQ ID NO 128)

IHYRNASGIYHI (SEQ ID NO 224)

VPYRNASGIYHV (SEQ ID NO 84)

VNYRNASGIYHI (SEQ ID NO 225)

VNYRNASGVYHI (SEQ ID NO 226)

VNYHNTSGIYHL (SEQ ID NO 227)

QHYRNASGIYHV (SEQ ID NO 228)

QHYRNVSGFYHV (SEQ ID NO 229)

IHYRNASDGYYI (SEQ ID NO 230)

LQVKNTSSSYMV (SEQ ID NO 231)

Region V2 encompasses amino acids 213 to 223. The following unique sequences can be found in the V2 region as shown in Figure 5:

VYEADDVILHT (SEQ ID NO 85)

VYETEHHLHL (SEQ ID NO 129)

VYEADHHIMHL (SEQ ID NO 130)

VYETDHHILHL (SEQ ID NO 131)

VYEADNLILHA (SEQ ID NO 86)

VWQLRAIVLHV (SEQ ID NO 232)

VYEADYHILHL (SEQ ID NO 233)

VYETDNHILHL (SEQ ID NO 234)

VYETENHILHL (SEQ ID NO 235)

VFETVHHILHL (SEQ ID NO 236)

VFETEHHLHL (SEQ ID NO 237)

VFETDHHIMHL (SEQ ID NO 238)

VYETENHILHL (SEQ ID NO 239)

VYEADALILHA (SEQ ID NO 240)

Region V3 encompasses the amino acids 230 to 242. The following unique V3 region sequences can be deduced from Figure 5:

VQDGNTSTCWTPV (SEQ ID NO 87)

VQDGNTSACWTPV (SEQ ID NO 241)

VRVGNQSRCWVAL (SEQ ID NO 132)

VRTGNTSRCWVPL (SEQ ID NO 133)

VRAGNVSRCWTPV (SEQ ID NO 134)

EEKGNISRCWIPV (SEQ ID NO 242)

VKTGNQSRCWVAL (SEQ ID NO 243)

VRTGNQSRCWVAL (SEQ ID NO 244)

VKTGNQSRCWIAL (SEQ ID NO 245)

VKTGNVSRCWIPL (SEQ ID NO 247)

VKTGNVSRCWISL (SEQ ID NO 248)

VRKDNVSRCWVQI (SEQ ID NO 249)

Region V4 encompasses the amino acids 248 to 257. The following unique V4 region sequences can be deduced from figure 5:

VRYVGATTAS (SEQ ID NO 89)
APYIGAPLES (SEQ ID NO 135)
APYVGAPLES (SEQ ID NO 136)
AVSMDAPLES (SEQ ID NO 137)
APSLGAVTAP (SEQ ID NO 90)
APSFGAVTAP (SEQ ID NO 250)
VSQPGALTKG (SEQ ID NO 251)
VKYVGATTAS (SEQ ID NO 252)
APYIGAPVES (SEQ ID NO 253)
AQHLNAPLES (SEQ ID NO 254)
SPYVGAPLEP (SEQ ID NO 255)
SPYAGAPLEP (SEQ ID NO 256)
APYLGAPLEP (SEQ ID NO 257)
APYLGAPLES (SEQ ID NO 258)
APYVGAPLES (SEQ ID NO 259)
VPYLGAPLTS (SEQ ID NO 260)
APHLRAPLSS (SEQ ID NO 261)
APYLGAPLTS (SEQ ID NO 262)

Region V5 encompasses the amino acids 294 to 303. The following unique V5 region peptides can be deduced from figure 5:

RPRRHQTQQT (SEQ ID NO 91)
QPRRHWTTQD (SEQ ID NO 138)
RPRRHWTQD (SEQ ID NO 139)
RPRQHATVQN (SEQ ID NO 92)
RPRQHATVQD (SEQ ID NO 263)
SPQHHKFVQD (SEQ ID NO 264)
RPRRLWTTQE (SEQ ID NO 265)
PPRIHETTQD (SEQ ID NO 266)

The variable region in the E2 region (HVR-2) of type 5a as shown in Figure 12 spanning amino acid positions 471 to 484 is also a preferred peptide according to the present invention

with the following sequence:

TISYANGSGPSDDK (SEQ ID NO 267)

The above given list of peptides are particularly suitable for vaccine and diagnostic development.

Also comprised in the present invention is any synthetic peptide or polypeptide containing at least 5 contiguous amino acids derived from the above-defined peptides in their peptidic chain.

According to a specific embodiment, the present invention relates to a composition as defined above, wherein said contiguous sequence is selected from any of the following HCV amino acid type 3 sequences:

- a sequence having a homology of more than 72%, preferably more than 74%, more preferably more than 77% and most preferably more than 80 or 84% homology to any of the amino acid sequences as represented in SEQ ID NO 14, 16, 18, 20, 22, 24, 26 or 28 (HD10, BR36, BR33 sequences) in the region spanning positions 140 to 319 in the Core/E1 region as shown in Figure 5;
- a sequence having a homology of more than 70%, preferably more than 72%, more preferably more than 75% homology, most preferably more than 81% homology to any of the amino acid sequences as represented in SEQ ID NO 14, 16, 18, 20, 22, 24, 26 or 28 (HD10, BR36, BR33 sequences) in the E1 region spanning positions 192 to 319 as shown in Figure 5;
- a sequence having a homology of more than 86%, preferably more than 88%, and most preferably more than 90% homology to the amino acid sequences as represented in SEQ ID NO 148 (type 3c); BE98 in the region spanning positions 1 to 110 in the Core region as shown in Figure 5;
- a sequence having a homology of more than 76%, preferably more than 78%, most preferably more than 80% to any of the amino acid sequences as represented in SEQ ID NO 30, 32, 34, 36, 38 or 40 (HCC153, HD10, BR36 sequences) in the region spanning positions 1646 to 1764 in the NS3/NS4 region as shown in Figure 7 and 11;
- a sequence having a homology of more than 81%, preferably more than 83%, and most preferably more than 86% homology to any of the amino acid sequences as represented in SEQ ID NO 14, 16, 18, 20, 22, 24, 26 or 28 (HD10, BR36, BR33 sequences) in the region spanning positions 140 to 319 in the Core/E1 region as shown in Figure 5;
- a sequence having a homology of more than 81.5%, preferably more than 83%, and most

preferably more than 86% homology to any of the amino acid sequences as represented in SEQ ID NO 14, 16, 18, 20, 22, 24, 26 or 28 (HD10, BR36, BR33 sequences) in the E1 region spanning positions 192 to 319 as shown in Figure 5;

- a sequence having a homology of more than 86%, preferably more than 88%, most preferably more than 90% to the amino acid sequence as represented in SEQ ID NO 150; (*type 3c BE98*) in the region spanning positions 2645 to 2757 in the NS5B region as shown in Figure 2.

According to yet another embodiment, the present invention relates to a composition as defined above, wherein said contiguous sequence is selected from any of the following HCV amino acid type 4 sequences:

- a sequence having a homology of more than 80%, preferably more than 82%, most preferably more than 84% homology to any of the amino acid sequences as represented in SEQ ID NO 118, 120, and 122 (GB358, GB549, GB809 sequences) in the region spanning positions 127 to 319 of the Core/E1 region as shown in Figure 5;
- a sequence having a homology of more than 73%, preferably more than 75%, most preferably more than 78% homology in the E1 region spanning positions 192 to 319 to any of the amino acid sequences as represented in SEQ ID NO 118, 120, and 122 (GB358, GB549, GB809 sequences) in the region spanning positions 140 to 319 of the Core/E1 region as shown in Figure 5;
- a sequence having more than 85%, preferably more than 86%, most preferably more than 87% homology to any of the amino acid sequences as represented in SEQ ID NO 118, 120 or 122 (GB358, GB549, GB809 sequences) in the region spanning positions 192 to 319 of E1 as shown in Figure 5;
- a sequence showing more than 73 %, preferably more than 74 %, most preferably more than 75% homology to any of the amino acid sequences as represented in SEQ ID NO 106, 108, 110, 112, 114 or 116 (GB48, GB116, GB215, GB358, GB549, GB809 sequences) in the region spanning positions 2645 to 2757 of the NS5B region as shown in Figure 2;
- a sequence having any of the sequences as represented in SEQ ID NO 164 or 166 (GB809 and CAM600 sequences) in the Core/E1 region as shown in Figure 5;
- a sequence having any of the sequences as represented in SEQ ID NO 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188 or 190 (CAM600, GB809, CAMG22, CAMG27, GB549, GB438, CAR4/1205, CAR4/901, GB116, GB215, GB958, GB809-4 sequences) in the E1 region as shown in Figure 5;

- a sequence having any of the sequences as represented in SEQ ID NO 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212 (GB358, GB724, BE100, PC, CAM600, CAMG22, etc.) in the NS5B region.

The above-mentioned type 4 peptides polypeptides comprise at least an amino acid sequence selected from any HCV type 4 polyprotein with the exception of core sequence as disclosed by Simmonds et al. (1993, EG-29, see Figure 5).

According to yet another aspect, the present invention relates to a composition as defined above, wherein said contiguous sequence is selected from any of the following HCV amino acid type 5 sequences:

- a sequence having more than 93%, preferably more than 94%, most preferably more than 95% homology in the region spanning Core positions 1 to 191 to any of the amino acid sequences as represented in SEQ ID NO 42, 44, 46, 48, 50, 52 or 54 (PC sequences) and SEQ ID NO 152 (BE95) as shown in Figure 5;
- a sequence having more than 73%, preferably more than 74%, most preferably more than 76% homology in the region spanning E1 positions 192 to 319 to any of the amino acid sequences as represented in SEQ ID NO 42, 44, 46, 48, 50, 52 or 54 (PC sequences) as shown in Figure 5 ;
- a sequence having a more than 78%, preferably more than 80%, most preferably more than 83% homology to any of the amino acid sequences as represented in SEQ ID NO 42, 44, 46, 48, 50, 52, 54, 154, 156 (BE95, BE100) (PC sequences) in the region spanning positions 1 to 319 of the Core/E1 region as shown in Figure 5;
- a sequence having more than 90%, preferably more than 91%, most preferably more than 92% homology to any of the amino acid sequences represented in SEQ ID NO 56 to 58 (PC sequences) in the region spanning positions 1286 to 1403 of the NS3 region as shown in Figure 7 or 11;
- a sequence having more than 66%, more particularly 68%, most particularly 70% or more homology to any of the amino acid sequences as represented in SEQ ID NO 60 or 62 (PC sequences) in the region spanning positions 1646 to 1764 of the NS3/4 region as shown in Figure 7 or 11.

According to yet another embodiment, the present invention relates to a composition as defined above, wherein said contiguous sequence is selected from any of the following HCV amino acid type 2d sequences:

- a sequence having more than 83%, preferably more than 85%, most preferably more than

87% homology to the amino acid sequence as represented in SEQ ID NO 144 (NE92) in the region spanning positions 1 to 319 of the Core/E1 region as shown in Figure 5;

- a sequence having more than 79%, preferably more than 81%, most preferably more than 84% homology in the region spanning E1 positions 192 to 319 to the amino acid sequence as represented in SEQ ID NO 144 (NE92) as shown in Figure 12;
- a sequence having more than 95%, more particularly 96%, most particularly 97% or more homology to the amino acid sequence as represented in SEQ ID NO 146 (NE92) in the region spanning positions 2645 to 2757 of the NS5B region as shown in Figure 2.

The present invention also relates to a recombinant vector, particularly for cloning and/or expression, with said recombinant vector comprising a vector sequence, an appropriate prokaryotic, eukaryotic or viral promoter sequence followed by the nucleotide sequences as defined above, with said recombinant vector allowing the expression of any one of the HCV type 2 and/or HCV type 3 and/or type 4 and/or type 5 derived polypeptides as defined above in a prokaryotic, or eukaryotic host or in living mammals when injected as naked DNA, and more particularly a recombinant vector allowing the expression of any of the following HCV type 2d, type 3, type 4 or type 5 polypeptides spanning the following amino acid positions:

- a polypeptide starting at position 1 and ending at any position in the region between positions 70 and 326, more particularly a polypeptide spanning positions 1 to 70, 1 to 85, positions 1 to 120, positions 1 to 150, positions 1 to 191, positions 1 to 200, for expression of the Core protein, and a polypeptide spanning positions 1 to 263, positions 1 to 326, for expression of the Core and E1 protein;
- a polypeptide starting at any position in the region between positions 117 and 192, and ending at any position in the region between positions 263 and 326, for expression of E1, or forms that have the putative membrane anchor deleted (positions 264 to 293 plus or minus 8 amino acids);
- a polypeptide starting at any position in the region between positions 1556 and 1688, and ending at any position in the region between positions 1739 and 1764, for expression of the NS4 regions, more particularly a polypeptide starting at position 1658 and ending at position 1711 for expression of the NS4a antigen, and more particularly, a polypeptide starting at position 1712 and ending between positions 1743 and 1972, for example 1712-1743, 1712-1764, 1712-1782, 1712-1972, 1712 to 1782 and 1902 to 1972 for expression of the NS4b protein or parts thereof.

The term "vector" may comprise a plasmid, a cosmid, a phage, or a virus.

In order to carry out the expression of the polypeptides of the invention in bacteria such as *E. coli* or in eukaryotic cells such as in *S. cerevisiae*, or in cultured vertebrate or invertebrate hosts such as insect cells, Chinese Hamster Ovary (CHO), COS, BHK, and MDCK cells, the following steps are carried out:

- transformation of an appropriate cellular host with a recombinant vector, in which a nucleotide sequence coding for one of the polypeptides of the invention has been inserted under the control of the appropriate regulatory elements, particularly a promoter recognized by the polymerases of the cellular host and, in the case of a prokaryotic host, an appropriate ribosome binding site (RBS), enabling the expression in said cellular host of said nucleotide sequence. In the case of an eukaryotic host any artificial signal sequence or pre/pro sequence might be provided, or the natural HCV signal sequence might be employed, e.g. for expression of E1 the signal sequence starting between amino acid positions 117 and 170 and ending at amino acid position 191 can be used, for expression of NS4, the signal sequence starting between amino acid positions 1646 and 1659 can be used,
- culture of said transformed cellular host under conditions enabling the expression of said insert.

The present invention also relates to a composition as defined above, wherein said polypeptide is a recombinant polypeptide expressed by means of an expression vector as defined above.

The present invention also relates to a composition as defined above, for use in a method for immunizing a mammal, preferably humans, against HCV comprising administering a sufficient amount of the composition possibly accompanied by pharmaceutically acceptable adjuvants, to produce an immune response, more particularly a vaccine composition including HCV type 3 polypeptides derived from the Core, E1 or the NS4 region and/or HCV type 4 and/or HCV type 5 polypeptides and/or HCV type 2d polypeptides.

The present invention also relates to an antibody raised upon immunization with a composition as defined above by means of a process as defined above, with said antibody being reactive with any of the polypeptides as defined above, and with said antibody being preferably a monoclonal antibody.

The monoclonal antibodies of the invention can be produced by any hybridoma liable to be formed according to classical methods from splenic cells of an animal, particularly from

a mouse or rat, immunized against the HCV polypeptides according to the invention, or muteins thereof, or fragments thereof as defined above on the one hand, and of cells of a myeloma cell line on the other hand, and to be selected by the ability of the hybridoma to produce the monoclonal antibodies recognizing the polypeptides which has been initially used for the immunization of the animals.

The antibodies involved in the invention can be labelled by an appropriate label of the enzymatic, fluorescent, or radioactive type.

The monoclonal antibodies according to this preferred embodiment of the invention may be humanized versions of mouse monoclonal antibodies made by means of recombinant DNA technology, departing from parts of mouse and/or human genomic DNA sequences coding for H and L chains or from cDNA clones coding for H and L chains.

Alternatively the monoclonal antibodies according to this preferred embodiment of the invention may be human monoclonal antibodies. These antibodies according to the present embodiment of the invention can also be derived from human peripheral blood lymphocytes of patients infected with type 3, type 4 or type 5 HCV, or vaccinated against HCV. Such human monoclonal antibodies are prepared, for instance, by means of human peripheral blood lymphocytes (PBL) repopulation of severe combined immune deficiency (SCID) mice (for recent review, see Duchosal et al. 1992).

The invention also relates to the use of the proteins of the invention, muteins thereof, or peptides derived therefrom for the selection of recombinant antibodies by the process of repertoire cloning (Persson et al., 1991).

Antibodies directed to peptides derived from a certain genotype may be used either for the detection of such HCV genotypes, or as therapeutic agents.

The present invention also relates to the use of a composition as defined above for incorporation into an immunoassay for detecting HCV, present in biological sample liable to contain it, comprising at least the following steps:

- (i) contacting the biological sample to be analyzed for the presence of HCV antibodies with any of the compositions as defined above preferably in an immobilized form under appropriate conditions which allow the formation of an immune complex, wherein said polypeptide can be a biotinylated polypeptide which is covalently bound to a solid substrate by means of streptavidin or avidin complexes,
- (ii) removing unbound components,
- (iii) incubating the immune complexes formed with heterologous antibodies, which

specifically bind to the antibodies present in the sample to be analyzed, with said heterologous antibodies having conjugated to a detectable label under appropriate conditions,

- (iv) detecting the presence of said immune complexes visually or by means of densitometry and inferring the HCV serotype present from the observed hybridization pattern.

The present invention also relates to the use of a composition as defined above, for incorporation into a serotyping assay for detecting one or more serological types of HCV present in a biological sample liable to contain it, more particularly for detecting E1 and NS⁴ antigens or antibodies of the different types to be detected combined in one assay format, comprising at least the following steps:

- (i) contacting the biological sample to be analyzed for the presence of HCV antibodies or antigens of one or more serological types, with at least one of the compositions as defined above, an immobilized form under appropriate conditions which allow the formation of an immune complex,
- (ii) removing unbound components,
- (iii) incubating the immune complexes formed with heterologous antibodies, which specifically bind to the antibodies present in the sample to be analyzed, with said heterologous antibodies having conjugated to a detectable label under appropriate conditions,
- (iv) detecting the presence of said immune complexes visually or by means of densitometry and inferring the presence of one or more HCV serological types present from the observed binding pattern.

The present invention also relates to the use of a composition as defined above, for immobilization on a solid substrate and incorporation into a reversed phase hybridization assay, preferably for immobilization as parallel lines onto a solid support such as a membrane strip, for determining the presence or the genotype of HCV according to a method as defined above.

The present invention thus also relates to a kit for determining the presence of HCV genotypes as defined above present in a biological sample liable to contain them, comprising:

- possibly at least one primer composition containing any primer selected from those defined above or any other HCV type 3 and/or HCV type 4, and/or HCV type 5, or universal HCV primers,

- at least one probe composition as defined above, with said probes being preferentially immobilized on a solid substrate, and more preferentially on one and the same membrane strip,
- a buffer or components necessary for producing the buffer enabling hybridization reaction between these probes and the possibly amplified products to be carried out,
- means for detecting the hybrids resulting from the preceding hybridization,
- possibly also including an automated scanning and interpretation device for inferring the HCV genotypes present in the sample from the observed hybridization pattern.

The genotype may also be detected by means of a type-specific antibody as defined above, which is linked to any polynucleotide sequence that can afterwards be amplified by PCR to detect the immune complex formed (Immuno-PCR. Sano et al., 1992);

The present invention also relates to a kit for determining the presence of HCV antibodies as defined above present in a biological sample liable to contain them, comprising:

- at least one polypeptide composition as defined above, preferentially in combination with other polypeptides or peptides from HCV type 1, HCV type 2 or other types of HCV, with said polypeptides being preferentially immobilized on a solid substrate, and more preferentially on one and the same membrane strip,
- a buffer or components necessary for producing the buffer enabling binding reaction between these polypeptides and the antibodies against HCV present in the biological sample,
- means for detecting the immunocomplexes formed in the preceding binding reaction,
- possibly also including an automated scanning and interpretation device for inferring the HCV genotypes present in the sample from the observed binding pattern.

Figure LegendsFigure 1

Alignment of consensus nucleotide sequences for each of the type 3a isolates BR34, BR36, and BR33, deduced from the clones with SEQ ID NO 1, 5, 9; type 4 isolates GB48, GB116, GB215, GB358, GB549, GB809, CAM600, CAMG22, GB438, CAR4/1205, CAR1/501 (SEQ ID NO. 106, 108, 110, 112, 114, 116, 201, 203, 205, 207, 209 and 211); type 5a isolates BE95 and BE96 (SEQ ID NO 159 and 161) and type 2d isolate NE92 (SEQ ID NO 145) from the region between nucleotides 7932 and 8271, with known sequences from the corresponding region of isolates HCV-1, HCV-J, HC-J6, HC-J8, T1 and T9, and others as shown in Table 3.

Figure 2

Alignment of amino acids sequences deduced from the nucleic acid sequences as represented in Figure 1 from the subtype 3a clones BR34 (SEQ ID NO 2, 4), BR36 (SEQ ID NO 6, 8) and BR33 (SEQ ID NO 10, 12), the subtype 3c clone BE98 (SEQ ID NO 150), and the type 4 clones GB48 (SEQ ID NO 107), GB116 (SEQ ID NO 109), GB215 (SEQ ID NO 111), GB358 (SEQ ID NO 113), GB549 (SEQ ID NO 115) GB809 (SEQ ID NO 117); CAM600, CAMG22, GB438, CAR4/1205, CAR1/501 (SEQ ID NO 202, 204, 206, 208, 210, 212); the type 5a clones BE95 and BE96 (SEQ ID NO 160 and 162); as well as the subtype 2d isolate NE92 (SEQ ID NO 146) from the region between amino acids 2645 to 2757 with known sequences from the corresponding region of isolates HCV-1, HCV-J, HC-J6, and HC-J8, T1 and T9, and other sequences as shown in Table 3.

Figure 3

Alignment of type 2d, 3c, 4 and 5a nucleotide sequences from isolates NE92, BE98, GB358, GB809, CAM600, GB724, BE95 (SEQ ID NO 143, 147, 191, 163, 165, 193 and 151) in the Core region between nucleotide positions 1 and 500, with known sequences from the corresponding region of type 1, type 2, type 3 and type 4 sequences.

Figure 4

Alignment of nucleotide sequences for the subtype 2d isolate NE92 (SEQ ID NO 143), the type 4 isolates GB358 (SEQ ID NO 118 and 187), GB549 (SEQ ID NO 120 and 175), and

GB809-2 (SEQ ID NO 122 and 169), GB 809-4, BG116, GB215, CAM600, CAMG22, CAMG27, GB438, CAR4/1205, CAR4/901 (SEQ ID NO 189, 183, 185, 167, 171, 173, 177, 179, 181), sequences for each of the subtype 3a isolates HD10, BR36, and BR33, (SEQ ID NO 13, 15, 17 (HD10), 19, 21 (BR36) and 23, 25 or 27 (BR23) and the subtype 5a isolates BE95 and BE100 (SEQ ID NO 143 and 195) from the region between nucleotides 379 and 957, with known sequences from the corresponding region of type 1 and 2 and 3.

Figure 5

Alignment of amino acid sequences deduced from the new HCV nucleotide sequences of the Core/E1 region of isolates BR33, BR36, HD10, GB358, GB549, and GB809, PC or BE95, CAM600, and GB724 (SEQ ID NO. 14, 20, 24, 119 or 192, 121, 123 or 164, 54 or 152, 166 and 194) from the region between positions 1 and 319, with known sequences from type 1a (HCV-1), type 1b (HCV-J), type 2a (HC-JG), type 2b (HC-J8), NZL1, HCV-TR, positions 7-89 of type 3a (E-b1), and positions 8-88 of type 4a (EG-29). V-Core, variable region with type-specific features in the core protein, V1, variable region 1 of the E1 protein, V2, variable region 2 of the E1 protein, V3, variable region 3 of the E1 protein, V4, variable region 4 of the E1 protein, V5, variable region 5 of the E1 protein.

Figure 6

Alignment of nucleotide sequences of isolates HCCL53, HD10 and BR36, deduced from clones with SEQ ID NO 29, 31, 33, 35, 37 and 39, from the NS3/4 region between nucleotides 4664 to 5292, with known sequences from the corresponding region of isolates HCV-1, HCV-J, HC-J6, and HC-J8, EB1, EB2, EB6 and EB7.

Figure 7

Alignment of amino acid sequences deduced from the new HCV nucleotide sequences of the NS3/NS4 region of isolate BR36 (SEQ ID NO 36, 38 and 40) and BE95 (SEQ ID NO 270). NS4-1, indicates the region that was synthesized as synthetic peptide 1 of the NS4 region, NS4-5, indicates the region that was synthesized as synthetic peptide 5 of the NS4 region; NS4-7, indicates the region that was synthesized as synthetic peptide 7 of the NS4 region.

Figure 8

Reactivity of the three LIPA-selected (Stuyver et al., 1993) type 3 sera on the Inno-LIA HCV Ab II assay (Innogenetics) (left), and on the NS4-LIA test. For the NS4-LIA test, NS4-1, NS4-5, and NS4-7 peptides were synthesized based on the type 1 (HCV-1), type 2 (HC-J6) and type 3 (BR36) prototype isolate sequences as shown in Table 4, and applied as parallel lines onto a membrane strip as indicated. 1, serum BR33, 2, serum HD10, 3, serum DKH.

Figure 9

Nucleotide sequences of Core/E1 clones obtained from the PCR fragments PC-2, PC-3, and PC-4, obtained from serum BE95 (PC-2-1 (SEQ ID NO 41), PC-2-6 (SEQ ID NO 43), PC-4-1 (SEQ ID NO 45), PC-4-6 (SEQ ID NO 47), PC-3-4 (SEQ ID NO 49), and PC-3-8 (SEQ ID NO 51)) of subtype 5a isolate BE95.

A consensus sequence is shown for the Core and E1 region of isolate BE95, presented as PC C/E1 with SEQ ID NO 53. Y, C or T, R, A or G, S, C or G.

Figure 10

Alignment of nucleotide sequences of clones with SEQ ID NO 197 and 199 (PC sequences, see also SEQ ID NO 55, 57, 59) and SEQ ID NO 35, 37 and 39 (BR36 sequences) from the NS3/4 region between nucleotides 3856 to 5292, with known sequences from the corresponding region of isolates HCV-1, HCV-J, HC-J6, and HC-J8.

Figure 11

Alignment of amino acid sequences of subtype 5a BE95 isolate PC clones with SEQ ID NO 56 and 58, from the NS3/4 region between amino acids 1286 to 1764, with known sequences from the corresponding region of isolates HCV-1, HCV-J, HC-J6, and HC-J8.

Figure 12

Alignment of amino acid sequences of subtype 5a isolate BE95 (SEQ ID NO 158) in the E1/E2 region spanning positions 328 to 546, with known sequences from the corresponding region of isolates HCV-1, HCV-J, HC-J6, HC-J8, NZL1 and HCV-TR (see Table 3).

Figure 13

Alignment of the nucleotide sequences of subtype 5a isolate BE95 (SEQ ID NO 157) in the E1/E2 region with known HCV sequences as shown in Table 3.

EXAMPLESExample 1: The NS5b region of HCV type 3

Type 3 sera, selected by means of the INNO-LiPA HCV research kit (Stuyver et al., 1993) from a number of Brazilian blood donors, were positive in the HCV antibody ELISA (Innotest HCV Ab II; Innogenetics) and/or in the INNO-LIA HCV Ab II confirmation test (Innogenetics). Only those sera that were positive after the first round of PCR reactions (Stuyver et al., 1993) were retained for further study.

Reverse transcription and nested PCR: RNA was extracted from 50 µl serum and subjected to cDNA synthesis as described (Stuyver et al., 1993). This cDNA was used as template for PCR, for which the total volume was increased to 50 µl containing 10 pmoles of each primer, 3 µl of 10x Pfu buffer 2 (Stratagene) and 2.5 U of Pfu DNA polymerase (Stratagene). The cDNA was amplified over 45 cycles consisting of 1 min 94°C, 1 min 50°C and 2 min 72°C. The amplified products were separated by electrophoresis, isolated, cloned and sequenced as described (Stuyver et al., 1993).

Type 3a and 3b-specific primers in the NS5 region were selected from the published sequences (Mori et al., 1992) as follows:

for type 3a:

HCPr161(+): 5'-ACCGGAGGCCAGGAGAGTGATCTCCTCC-3' (SEQ ID NO 63) and
HCPr162(-): 5'-GGGCTGCTCTATCCTCATCGACGCCATC-3' (SEQ ID NO 64);

for type 3b:

HCPr163(+): 5'-GCCAGAGGCTCGGAAGGCGATCAGCGCT-3' (SEQ ID NO 65) and
HCPr164(-): 5'-GAGCTGCTCTGTCCTCCTCGACGCCGCA-3' (SEQ ID NO 66)

Using the Line Probe Assay (LiPA) (Stuyver et al., 1993), seven high-titer type 3 sera were selected and subsequently analyzed with the primer sets HCPr161/162 for type 3a, and HCPr163/164 for type 3b. None of these sera was positive with the type 3b primers. NS5 PCR fragments obtained using the type 3a primers from serum BR36 (BR36-23), serum BR33 (BR33-2) and serum BR34 (BR34-4) were selected for cloning. The following sequences were obtained from the PCR fragments :

From fragment BR34-4:

BR34-4-20 (SEQ ID NO 1), BR34-4-19 (SEQ ID NO 3)

From fragment BR36-23:

BR36-23-18 (SEQ ID NO 5), BR36-23-20 (SEQ ID NO 7)

From fragment BR33-2:

BR33-2-17 (SEQ ID NO 9), BR33-2-21 (SEQ ID NO 11)

An alignment of sequences with SEQ ID NO 1, 5 and 9 with known sequences is given in Figure 1. An alignment of the deduced amino acid sequences is shown in Figure 2. The 3 isolates are very closely related to each other (mutual homologies of about 95 %) and to the published sequences of type 3a (Mori et al., 1992), but are only distantly related to type 1 and type 2 sequences (Table 5). Therefore, it is clearly demonstrated that NS5 sequences from LiPA-selected type 3 sera are indeed derived from a type 3 genome. Moreover, by analyzing the NS5 region of serum BR34, for which no 5'UR sequences were determined as described in Stuyver et al. (1993), the excellent correlation between typing by means of the LiPA and genotyping as deduced from nucleotide sequencing was further proven.

Example 2: The Core/E1 region of HCV type 3

After aligning the sequences of HCV-1 (Choo et al., 1991), HCV-J (Kato et al., 1990), HC-J6 (Okamoto et al., 1991), and HC-J8 (Okamoto et al., 1992), PCR primers were chosen in those regions of little sequence variation. Primers HCP23(+): 5'-CTCATGGGGTACATTCCGCT-3' (SEQ ID NO 67) and HCP54(-): 5'-TATTACCAGTTCATCATCATATCCCA-3' (SEQ ID NO 68), were synthesized on a 392 DNA/RNA synthesizer (Applied Biosystems). This set of primers was selected to amplify the sequence from nucleotide 397 to 957 encoding amino acids 140 to 319 (Kato et al., 1990): 52 amino acids from the carboxyterminus of core and 128 amino acids of E1 (Kato et al., 1990). The amplification products BR36-9, BRR33-1, and HD10-2 were cloned as described (Stuyver et al., 1993). The following clones were obtained from the PCR fragments:

From fragment HD10-2:

HD10-2-5 (SEQ ID NO 13), HD10-2-14 (SEQ ID NO 15), HD10-2-21 (SEQ ID NO 17)

From fragment BR36-9:

BR36-9-13 (SEQ ID NO 19), BR36-9-20 (SEQ ID NO 21),

From fragment BR33-1:

BR33-1-10 (SEQ ID NO 23), BR33-1-19 (SEQ ID NO 25), BR33-1-20 (SEQ ID NO 27).

An alignment of the type 3 E1 nucleotide sequences (HD10, BR36, BR33) with SEQ ID NO 13, 19 and 23 with known E1 sequences is presented in Figure 4. Four variations were detected in the E1 clones from serum HD10 and BR36, while only 2 were found in BR33. All are silent third letter variations, with the exception of mutations at position 40 (L to P)

and 125 (M to I). The homologies of the type 3 E1 region (without core) with type 1 and 2 prototype sequences are depicted in Table 5.

In total, 8 clones covering the core/E1 region of 3 different isolates were sequenced and the E1 portion was compared with the known genotypes (Table 3) as shown in Figure 5. After computer analysis of the deduced amino acid sequence, a signal-anchor sequence at the core carboxyterminus was detected which might, through analogy with type 1b (Hijikata et al., 1991), promote cleavage before the LEWRN sequence (position 192, Fig. 5). The L-to-P mutation in one of the HD10-2 clones resides in this signal-anchor region and potentially impairs recognition by signal peptidase (computer prediction). Since no examples of such substitutions were found at this position in previously described sequences, this mutation might have resulted from reverse transcriptase or *Pfu* polymerase misincorporation. The 4 amino-terminal potential N-linked glycosylation sites, which are also present in HCV types 1a and 2, remain conserved in type 3. The N-glycosylation site in type 1b (aa 250, Kato et al., 1990) remains a unique feature of this subtype. All E1 cysteines, and the putative transmembrane region (aa 264 to 293, computer prediction) containing the aspartic acid at position 279, are conserved in all three HCV types. The following hypervariable regions can be delineated: V1 from aa 192 to 203 (numbering according to Kato et al., 1990), V2 (213-223), V3 (230-242), V4 (248-257), and V5 (294-303). Such hydrophilic regions are thought to be exposed to the host defense mechanisms. This variability might therefore have been induced by the host's immune response. Additional putative N-linked glycosylation sites in the V4 region in all type 1b isolates known today and in the V5 region of HC-J8 (type 2b) possibly further contribute to modulation of the immune response. Therefore, analysis of this region, in the present invention, for type 3 and 4 sequences has been instrumental in the delineation of epitopes that reside in the V-regions of E1, which will be critical for future vaccine and diagnostics development.

Example 3: The NS3/NS4 region of HCV Type 3

For the NS3/NS4 border region, the following sets of primers were selected in the regions of little sequence variability after aligning the sequences of HCV-1 (Choo et al., 1991), HCV-J (Kato et al., 1990), HC-J6 (Okamoto et al., 1991), and HC-J8 (Okamoto et al., 1992) (smaller case lettering is used for nucleotides added for cloning purposes):

set A:

HCP116(+): 5'-tttAAATACATCATGRCITGYATG-3' (SEQ ID NO 69)

HCPr66 (-): 5'-ctattaTTGTATCCRCTGATGAARTTCCACAT-3' (SEQ ID NO 70)

set B:

HCPr116(+): 5'-ttttAAATACATCATGRCITGYATG-3' (SEQ ID NO 69)

HCPr118(-): 5'-actagtcgactaYTGIATICCRCTIATRWARTTCCACAT-3' (SEQ ID NO 71)

set C:

HCPr117(+): 5'-ttttAAATACATCGCIRCITGCATGCA-3' (SEQ ID NO 72)

HCPr66 (-): 5'-ctattaTTGTATCCRCTGATGAARTTCCACAT-3' (SEQ ID NO 70)

set D:

HCPr117(+): 5'-ttttAAATACATCGCIRCITGCATGCA-3' (SEQ ID NO 72)

HCPr118(-): 5'-actagtcgactaYTGIATICCRCTIATRWARTTCCACAT-3' (SEQ ID NO 71)

set E:

HCPr116(+): 5'-ttttAAATACATCATGRCITGYATG-3' (SEQ ID NO 69)

HCPr119(-): actagtcgactaRTTIGCIATIAGCCG/TRTTCATCCA YTG-3' (SEQ ID NO 73)

set F:

HCPr117(+): 5'-ttttAAATACATCGCIRCITGCATGCA-3' (SEQ ID NO 72)

HCPr119(-): actagtcgactaRTTIGCIATIAGCCG/TRTTCATCCA YTG-3' (SEQ ID NO 73)

set G:

HCPr131(+): 5'-ggaattctagaCCITCITGGGAYGARAYITGGAARTG-3' (SEQ ID NO 74)

HCPr66 (-): 5'-ctattaTTGTATCCRCTGATGAARTTCCACAT-3' (SEQ ID NO 70)

set H:

HCPr130(+): 5'-ggaattctagACIGCITAYCARGCIACIGTITGYGC-3' (SEQ ID NO 75)

HCPr66 (-): 5'-ctattaTTGTATCCRCTGATGAARTTCCACAT-3' (SEQ ID NO 70)

set I:

HCPr134(+): 5'-CATATAGATGCCCACTTCCTATC-3' (SEQ ID NO 76)

HCPr66 (-): 5'-ctattaTTGTATCCRCTGATGAARTTCCACAT-3' (SEQ ID NO 70)

set J:

HCPr131(+): 5'-ggaattctagaCCITCITGGGAYGARAYITGGAARTG-3' (SEQ ID NO 74)

HCPr118(-): 5'-actagtcgactaYTGIATICCRCTIATRWARTTCCACAT-3' (SEQ ID NO

71)

set K:

HCPr130(+): 5'-ggaattctagACIGCITAYCARGCIACIGTITGYGC-3' (SEQ ID NO 75)

HCPr118(-): 5'-actagtcgactaYTGIATICCRCTIATRWARTTCCACAT-3' (SEQ ID NO

71)

set L:

HCPr134(+): 5'-CATATAGATGCCCACTTCCTATC-3' (SEQ ID NO 76)

HCPr118(-): 5'-actagtgcacta YTGIATICCRCTIATRWARTTCCACAT-3' (SEQ ID NO 71)

set M:

HCPr3(+): 5'-GTGTGCCAGGACCATC-3' (SEQ ID NO 77) and

HCPr4(-): 5'-GACATGCATGTCATGATGTA-3 (SEQ ID NO 78)

set N:

HCPr3(+): 5'-GTGTGCCAGGACCATC-3' (SEQ ID NO 77) and

HCPr118(-): 5'-actagtgcacta YTGIATICCRCTIATRWARTTCCACAT-3' (SEQ ID NO 71)

set O:

HCPr3(+): 5'-GTGTGCCAGGACCATC-3' (SEQ ID NO 77) and

HCPr66 (-): 5'-cataTTGTATCCCCTGATGAARTTCCACAT-3' (SEQ ID NO 70)

No PCR products could be obtained with the sets of primers A, B, C, D, E, F, G, H, I, J, K, L, M, and N, on random-primed cDNA obtained from type 3 sera. With the primer set O, no fragment could be amplified from type 3 sera. However, a smear containing a few weakly stainable bands was obtained from serum BR36. After sequence analysis of several DNA fragments, purified and cloned from the area around 300 bp on the agarose gel, only one clone, HCCI53 (SEQ ID NO 29), was shown to contain HCV information. This sequence was used to design primer HCPr152.

A new primer set P was subsequently tested on several sera.

set P:

HCPr152(+): 5'-TACGCCTCTTCTATATCGGTTGGGCCTG-3' (SEQ ID NO 79) and

HCPr66(-): 5'-CTATTATTGTATCCCCTGATGAARTTCCACAT-3' (SEQ ID NO 70)

The 464-bp HCPr152/66 fragment was obtained from serum BR36 (BR36-20) and serum HD10 (HD10-1). The following clones were obtained from these PCR products:

From fragment HD10-1:

HD10-1-25 (SEQ ID NO 31), HD10-1-3 (SEQ ID NO 33),

From fragment BR36-20:

BR36-20-164 (SEQ ID NO 35), BR36-20-165 (SEQ ID NO 37), BR36-20-166 (SEQ ID NO 39),

The nucleotide sequences obtained from clones with SEQ ID NO 29, 31, 33, 35, 37 or 39 are shown aligned with the sequences of prototype isolates of other types of HCV in Figure 6. In addition to one silent 3rd letter variation, one 2nd letter mutation resulted in an

E to G substitution at position 175 of the deduced amino acid sequence of BR36 (Fig. 7). Serum HD10 clones were completely identical. The two type 3 isolates were nearly 94% homologous in this NS4 region. The homologies with other types are presented in Table 5.

Example 4: Analysis of the anti-NS4 response to type-specific peptides

As the NS4 sequence contains the information for an important epitope cluster, and since antibodies towards this region seem to exhibit little cross-reactivity (Chan et al., 1991), it was worthwhile to investigate the type-specific antibody response to this region. For each of the 3 genotypes, HCV-1 (Choo et al., 1991), HC-J6 (Okamoto et al., 1991) and BR36 (present invention), three 20-mer peptides were synthesized covering the epitope region between amino acids 1688 and 1743 (as depicted in table 6). The synthetic peptides were applied as parallel lines onto membrane strips. Detection of anti-NS4 antibodies and color development was performed according to the procedure described for the INNO-LIA HCV Ab II kit (Innogenetics, Antwerp). Peptide synthesis was carried out on a 9050 PepSynthesizer (Millipore). After incubation with 15 LiPA-selected type 3 sera, 9 samples showed reactivity towards NS4 peptides of at least 2 different types, but a clearly positive reaction was observed for 3 sera (serum BR33, HD30 and DKH) on the type 3 peptides, while negative (serum BR33 and HD30) or indeterminate (serum DKH) on the type 1 and type 2 NS4 peptides; 3 sera tested negative for anti-NS4 antibodies (Figure 8). Using the same membrane strips coated with the 9 peptides as indicated above and as shown in Figure 8, 38 type 1 sera (10 type 1a and 28 type 1b), 11 type 2 sera (10 type 2a and 1 type 2b), 12 type 3a sera and 2 type 4 sera (as determined by the LiPA procedure) were also tested. As shown in Table 8, the sera reacted in a genotype-specific manner with the NS4 epitopes. These results demonstrate that type-specific anti-NS4 antibodies can be detected in the sera of some patients. Such genotype-specific synthetic peptides might be employed to develop serotyping assays, for example a mixture of the nine peptides as indicated above, or combined with the NS4 peptides from the HCV type 4 or 6 genotype or from new genotypes corresponding to the region between amino acids 1688 and 1743, or synthetic peptides of the NS4 region between amino acids 1688 and 1743 of at least one of the 6 genotypes, combined with the E1 protein or deletion mutants thereof, or synthetic E1 peptides of at least one of the genotypes. Such compositions could be further extended with type-specific peptides or proteins, including for example the region between amino acids 68 and 91 of the core protein, or more preferably the region between amino acids 68 and 78. Furthermore, such type-specific

antigens may be advantageously used to improve current diagnostic screening and confirmation assays and/or HCV vaccines.

Example 5 The Core and E1 regions of HCV type 5

Sample BE95 was selected from a group of sera that reacted positive in a prototype Line Probe Assay as described earlier (Stuyver et al., 1993), because a high-titer of HCV RNA could be detected, enabling cloning of fragments by a single round of PCR. As no sequences from any coding region of type 5 has been disclosed yet, synthetic oligonucleotides for PCR amplification were chosen in the regions of little sequence variation after aligning the sequences of HCV-1 (Choo et al., 1991), HCV-J (Kato et al., 1990), HC-J6 (Okamoto et al., 1991), HC-J8 (Okamoto et al., 1992), and the new type 3 sequences of the present invention HD10, BR33, and BR36 (see Figure 5, Example 2). The following sets of primers were synthesized on a 392 DNA/RNA synthesizer (Applied Biosystems):

Set 1:

HCPr52(+): 5'-atgTTGGGTAAAGGTCATCGATAACCCT-3' (SEQ ID NO 80) and

HCPr54(-): 5'-ctattaCCAGTTCATCATCATATCCCC-3' (SEQ ID NO 78)

Set 2:

HCPr41(+): 5'-CCCGGGAGGTCTCGTAGACCGTGCA-3' (SEQ ID NO 81) and

HCPr40(-): 5'-ctattaAAGATAGAGAAAGAGCAACCGGG-3'(SEQ ID NO 82)

Set 3:

HCPr41(+): 5'-CCCGGGAGGTCTCGTAGACCGTGCA-3' (SEQ ID NO 81) and

HCPr54(-): 5'-ccattaCCAGTTCATCATCATATCCCC-3' (SEQ ID NO 78)

The three sets of primers were employed to amplify the regions of the type 5 isolate PC as described (Stuyver et al., 1993). Set 1 was used to amplify the E1 region and yielded fragment PC-4, set 2 was designed to yield the Core region and yielded fragment PC-2. Set 3 was used to amplify the Core and E1 region and yielded fragment PC-3. These fragments were cloned as described (Stuyver et al., 1993). The following clones were obtained from the PCR fragments:

From fragment PC-2:

PC-2-1 (SEQ ID NO 41), PC-2-6 (SEQ ID NO 43),

From fragment PC-4:

PC-4-1 (SEQ ID NO 45), PC-4-6 (SEQ ID NO 47),

From fragment PC-3:

PC-3-4 (SEQ ID NO 49), PC-3-8 (SEQ ID NO 51)

An alignment of sequences with SEQ ID NO 41, 43, 45, 47, 49 and 51, is given in Figure 9. A consensus amino acid sequence (PC C/E1; SEQ ID NO 54) can be deduced from each of the 2 clones cloned from each of the three PCR fragments as depicted in Figure 5, which overlaps the region between nucleotides 1 and 957 (Kato et al., 1990). The 6 clones are very closely related to each other (mutual homologies of about 99.7%).

An alignment of nucleotide sequence with SEQ ID NO 53 or 151 (PC C/E1 from isolate BE95) with known nucleotide sequences from the Core/E1 region is given in Figure 3. The clone is only distantly related to type 1, type 2, type 3 and type 4 sequences (Table 5).

Example 6: NS3/NS4 region of HCV type 5

Attempts were undertaken to clone the NS3/NS4 region of the isolate BE95, described in example 5. The following sets of primers were selected in the regions of little sequence variability after aligning the sequences of HCV-1 (Choo et al., 1991), HCV-J (Kato et al., 1991), HC-J6 (Okamoto et al., 1991), and HC-J8 (Okamoto et al., 1992) and of the sequences obtained from type 3 sera of the present invention (SEQ ID NO 31, 33, 35, 37 and 39); smaller case lettering is used for nucleotides added for cloning purposes:

set A:

HCP*r*116(+): 5'-ttttAAATACATCATGRCITGYATG-3' (SEQ ID NO 66)

HCP*r*66 (-): 5'-ctattaTTGTATCCRCTGATGAARTTCCACAT-3' (SEQ ID NO 70)

set B:

HCP*r*116(+): 5'-ttttAAATACATCATGRCITGYATG-3' (SEQ ID NO 69)

HCP*r*118(-): 5'-actagtgcactaYTGIATICCRCTIATRWARTTCCACAT-3' (SEQ ID NO 71)

set C:

HCP*r*117(+): 5'-ttttAAATACATCGCIRCITGCATGCA-3' (SEQ ID NO 72)

HCP*r*66 (-): 5'-ctattaTTGTATCCRCTGATGAARTTCCACAT-3' (SEQ ID NO 70)

set D:

HCP*r*117(+): 5'-ttttAAATACATCGCIRCITGCATGCA-3' (SEQ ID NO 72)

HCP*r*118(-): 5'-actagtgcactaYTGIATICCRCTIATRWARTTCCACAT-3' (SEQ ID NO 71)

set E:

HCP*r*116(+): 5'-ttttAAATACATCATGRCITGYATG-3' (SEQ ID NO 69)

HCP*r*119(-): actagtgcactaRTTIGCIATIAGCCG/TRTCATCCAYTG-3' (SEQ ID NO 73)

set F:

HCPr117(+): 5'-tttAAATACATCGCIRCITGCATGCA-3' (SEQ ID NO 72)

HCPr119(-): actagtcgactaRTTIGCIATIAGCCG/TRTTCATCCAYTG-3' (SEQ ID NO 73)

set G:

HCPr131(+): 5'-ggaattctagaCCITCITGGAYGARAYITGGAARTG-3' (SEQ ID NO 74)

HCPr66 (-): 5'-ctattaTTGTATCCCRCGTGATGAARTTCCACAT-3' (SEQ ID NO 70)

set H:

HCPr130(+): 5'-ggaattctagACIGCITAYCARGCIACIGTITGYGC-3' (SEQ ID NO 75)

HCPr66 (-): 5'-ctattaTTGTATCCCRCGTGATGAARTTCCACAT-3' (SEQ ID NO 70)

set I:

HCPr134(+): 5'-CATATAGATGCCCACTTCCTATC-3' (SEQ ID NO 76)

HCPr66 (-): 5'-ctattaTTGTATCCCRCGTGATGAARTTCCACAT-3' (SEQ ID NO 70)

set J:

HCPr131(+): 5'-ggaattctagaCCITCITGGAYGARAYITGGAARTG-3' (SEQ ID 74)

HCPr118(-): 5'-actagtcgactaYTGIATICCRCTIATRWARTTCCACAT-3' (SEQ ID NO 71)

set K:

HCPr130(+): 5'-ggaattctagACIGCITAYCARGCIACIGTITGYGC-3' (SEQ ID NO 75)

HCPr118(-): 5'-actagtcgactaYTGIATICCRCTIATRWARTTCCACAT-3' (SEQ ID NO 71)

set L:

HCPr134(+): 5'-CATATAGATGCCCACTTCCTATC-3' (SEQ ID NO 76)

HCPr118(-): 5'-actagtcgactaYTGIATICCRCTIATRWARTTCCACAT-3' (SEQ ID NO 71)

set M:

HCPr3(+): 5'-GTGTGCCAGGACCATC-3' (SEQ ID NO 77) and

HCPr4(-): 5'-GACATGCATGTCATGATGTA-3' (SEQ ID NO 78)

set N:

HCPr3(+): 5'-GTGTGCCAGGACCATC-3' (SEQ ID NO 77) and

HCPr118(-): 5'-actagtcgactaYTGIATICCRCTIATRWARTTCCACAT-3' (SEQ ID NO 71)

set O:

HCPr3(+): 5'-GTGTGCCAGGACCATC-3' (SEQ ID NO 77) and

HCPr66 (-): 5'-ctattaTTGTATCCCRCGTGATGAARTTCCACAT-3' (SEQ ID NO 70)

No PCR products could be obtained with the sets of primers A, B, C, D, E, F, G, H, I, J, K, L, M, and N, on random-primed cDNA obtained from type 3 sera. However,

set O yielded what appeared to be a PCR artifact fragment estimated about 1450 base pairs, instead of the expected 628 base pairs. Although it is not expected that PCR artifact fragments contain information of the gene or genome that was targetted in the experiment, efforts were put in cloning of this artifact fragment, which was designated fragment PC-1. The following clones, were obtained from fragment PC-1:

PC-1-37 (SEQ ID NO 59 and SEQ ID NO 55), PC-1-48 (SEQ ID NO 61 and SEQ ID NO 57)

The sequences obtained from the 5' and 3' ends of the clones are given in SEQ ID NOS 55, 57, 59, and 61, and the complete sequences with SEQ ID NO 197 and 199 are shown aligned with the sequences of prototype isolates of other types of HCV in Figure 10 and the alignment of the deduced amino acid sequences is shown in Figure 11 and 7. Surprisingly, the PCR artifact clone contained HCV information. The positions of the sequences within the HCV genome are compatible with a contiguous HCV sequence of 1437 nucleotides, which was the estimated size of the cloned PCR artifact fragment. Primer HCPr66 primed correctly at the expected position in the HCV genome. Therefore, primer HCPr3 must have incidentally misprimed at a position 809 nucleotides upstream of its legitimate position in the HCV genome. This could not be expected since no sequence information was available from a coding region of type 5.

Example 7 : The E2 region of HCV type 5

Serum BE95 was chosen for experiments aimed at amplifying a part of the E2 region of HCV type 5.

After aligning the sequences of HCV-1 (2), HCV-J(1), HC-J6 (3), and HC-J8 (4), PCR primers were chosen in those regions of little sequence variation.

Primers HCPr109(+): 5'-TGGGATATGATGATGAAGTC-3' (SEQ ID NO 141) and HCPr14(-): 5'-CCAGGTACAACCGAACCAATTGCC-3' (SEQ ID NO 142) were combined to amplify the aminoterminal region of the E2/NS1 region, and were synthesized on a 392 DNA/RNA synthesizer (Applied Biosystems). With primers HCPr109 and HCPr14, a PCR fragment of 661 bp was generated, containing 169 nucleotides corresponding to the E1 carboxyterminus and 492 bases from the region encoding the E2 aminotermminus.

An alignment of the type 5 E1/E2 sequences with seq ID NO. 158 with known sequences is presented in Figure 10. The deduced protein sequence was compared with the different

genotypes (Fig. 12, amino acids 328-546). In the E1 region, there were no extra structural important motifs found. The aminoterminal part of E2 was hypervariable when compared with the other genotypes. All 6 N-glycosylation sites and all 7 cysteine residue's were conserved in this E2 region. To preserve alignment, it was necessary to introduce a gap between aa 474 and 475 as for type 3a, but not between aa 480 and 481, as for type 2.

Example 8 : The NS5b region of HCV type 4

Type 4 sera GB48, GB116, GB215, and GB358, selected by means of the line probe assay (LiPA, Stuyver et al., 1993), as well as sera GB549 and GB809 that could not be typed by means of this LiPA (only hybridization was observed with the universal probes), were selected from Gabonese patients. All these sera were positive after the first round of PCR reactions for the 5' untranslated region (Stuyver et al., 1993) and were retained for further study.

RNA was isolated from the sera and cDNA synthesized as described in example 1.

Universal primers in the NS5 region were selected after alignment of the published sequences as follows:

HCPr206(+): 5'-TGGGGATCCCGTATGATAACCGCTGCTTGAA-3'
(SEQ ID NO. 124) and

HCPr207(-): 5'-GGCGGAATTCTGGTCATAGCCTCCGTGAA-3'
(SEQ ID NO. 125);

and were synthesized on a 392 DNA/RNA synthesizer (Applied Biosystems). Using the Line Probe Assay (LiPA), four high-titer type 4 sera and 2 sera that could not be classified were selected and subsequently analyzed with the primer set HCPr206/207. NS5 PCR fragments obtained using these primers from serum GB48 (GB48-3), serum GB116 (GB116-3), serum GB215 (GB215-3), serum GB358 (GB358-3), serum GB549 (GB549-3), and serum GB809 (GB809-3), were selected for cloning. The following sequences were obtained from the PCR fragments:

From fragment GB48-3 : GB48-3-10 (SEQ ID NO. 106)

From fragment GB116-3: GB116-3-5 (SEQ ID NO. 108)

From fragment GB215-3: GB215-3-8 (SEQ ID NO. 110)

From fragment GB358-3: GB358-3-3 (SEQ ID NO. 112)

From fragment GB549-3: GB549-3-6 (SEQ ID NO. 114)

From fragment GB809-3: GB809-3-1 (SEQ ID NO. 116)

An alignment of nucleotide sequences with SEQ ID NO. 106, 108, 110, 112, 114, and 116 with known sequences is given in Figure 1. An alignment of deduced amino acid sequences with SEQ ID NO. 107, 109, 111, 113, 115, and 117 with known sequences is given in Figure 2. The 4 isolates that had been typed as type 4 by means of LiPA are very closely related to each other (mutual homologies of about 95 %), but are only distantly related to type 1, type 2, and type 3 sequences (e.g. GB358 shows homologies of 65.6 to 67.7% with other genotypes, Table 4). The sequence obtained from sera GB549 and GB809 also show similar homologies with genotypes 1, 2, and 3 (65.9 to 68.8% for GB549 and 65.0 to 68.5% for GB809, Table 4), but an intermediate homology of 79.7 to 86.8% (often observed between subtypes of the same type) exists between GB549 or GB809 with the group of isolates consisting of GB48, GB116, GB215, and GB358, or between GB549 and GB809. These data indicate the discovery of 3 new subtypes within the HCV genotype 4: in the present invention, these 3 subtypes are designated subtype 4c, represented by isolates GB48, GB116, GB215, and GB358, subtype 4g, represented by isolate GB549, and subtype 4e, represented by isolate GB809. Although the homologies observed between subtypes in the NS5 region seem to indicate a closer relationship between subtypes 4c and 4e, the homologies observed in the E1 region indicate that subtypes 4g and 4e show the closest relation (see example 8).

Example 9 : The Core/E1 region of HCV type 4

From each of the 3 new type 4 subtypes, one representative serum was selected for cloning experiments in the Core/E1 region. GB549 (subtype 4g) and GB809 (subtype 4e) were analyzed together with isolate GB358 that was chosen from the subtype 4c group.

Synthetic oligonucleotides:

After aligning the sequences of HCV-1 (2), HCV-J(1), HC-J6 (3), and HC-J8 (4), PCR primers were chosen in those regions of little sequence variation.

Primers HCPr52(+): 5'-atgTTGGGTAAGGTACATCGATACCCT-3'; HCPr23(+): 5'-C T C A T G G G G T A C A T T C C G C T - 3', and HCPr54(-): 5' - CTATTACCAGTTCATCATCATATCCCA-3', were synthesized on a 392 DNA/RNA synthesizer (Applied Biosystems). The sets of primers HCPr23/54 and HCPr52/54 were used, but only with the primer set HCPr52/54, PCR fragments could be obtained. This set of primers amplified the sequence from nucleotide 379 to 957 encoding amino acids 127 to 319: 65 amino acids from the carboxyterminus of core and 128 amino acids of E1. The

amplification products GB358-4, GB549-4, and GB809-4 were cloned as described in example 1. The following clones were obtained from the PCR fragments:

From fragment GB358-4: GB358-4-1 (SEQ ID NO 118)

From fragment GB549-4: GB549-4-3 (SEQ ID NO 120)

From fragment GB809-4: GB809-4-3 (SEQ ID NO 122)

An alignment of the type 4 Core/E1 nucleotide sequences with seq ID NO. 118, 120, and 122 with known sequences is presented in Figure 4. The homologies of the type 4 E1 region (without core) with type 1, type 2, type 3, and type 5 prototype sequences are depicted in Table 4. Homologies of 53 to 66% are observed with representative isolates of non-type 4 genotypes. Observed homologies in the E1 region within type 4, between the different subtypes, ranges from 75.2 to 78.4%. The recently disclosed sequences of the core region of Egyptian type 4 isolates (for example EG-29 in Figure 3) described by Simmonds et al. (1993) do not allow alignment with the Gabonese sequences (as described in the present invention) in the NSB region and may belong to different type 4 subtype(s) as can be deduced from the core sequences. The deduced amino acid sequences with SEQ ID NO 119, 121, and 123 are aligned with other prototype sequences in Figure 5. Again, type-specific variation mainly resides in the variable V regions, designated in the present invention, and therefore, type-4-specific amino acids or V regions will be instrumental in diagnosis and therapeutics for HCV type 4.

Example 10 : The Core/E1 and NS5b regions of new HCV type 2, 3 and 4 subtypes

Samples NE92 (subtype 2d), BE98 (subtype 3c), CAM600 and GB809 (subtype 4e), CAMG22 and CAMG27 (subtype 4f), GB438 (subtype 4h), CAR4/1205 subtype (4i), CAR1/501 (subtype 4j), CAR1/901 (subtype 4?), and GB724 (subtype 4?) were selected from a group of sera that reacted positive but aberrantly in a prototype Line Probe Assay as described earlier (Stuyver et al., 1993). Another type 5a isolate BE100 was also analyzed in the C/E1 region, and yet another type 5a isolate BE96 in the NS5b region. A high-titer of HCV RNA could be detected, enabling cloning of fragments by a single round of PCR. As no sequences from any coding region of these subtypes had been disclosed yet, synthetic oligonucleotides for PCR amplification were chosen in the regions of little sequence variation after aligning the sequences of HCV-1 (Choo et al., 1991), HCV-J(Kato et al., 1990), HC-J6 (Okamoto et al., 1991), HC-J8 (Okamoto et al., 1992), and the other new sequences of the present invention.

The above mentioned sets 1, 2 and 3 (see example 5) of primers were used, but only with set 1, PCR fragments could be obtained from all isolates (except for BE98, GB724, and CAR1/501). This set of primers amplified the sequence from nucleotide 379 to 957 encoding amino acids 127 to 319: 65 amino acids from the carboxyterminus of core and 128 amino acids of E1. With set 3, the core/E1 region from isolate NE92 and BE98 could be amplified, and with set 2, the core region of GB358, GB724, GB809, and CAM600 could be amplified. The amplification products were cloned as described in example 1. The following clones were obtained from the PCR fragments:

From isolate GB724, the clone with SEQ ID NO 193 from the core region.

From isolate NE92, the clone with SEQ ID NO 143

From isolate BE98, the clone from the core/E1 region of which part of the sequence has been analyzed and is given in SEQ ID NO 147,

From isolate CAM600, the clone with SEQ ID NO 167 from the E1 region, or SEQ ID NO 165 from the Core/E1 region as shown in Figure 3,

From isolate CAMG22, the clone with SEQ ID NO 171 from the E1 region as shown in Figure 4,

from isolate GB358, the clone with SEQ ID NO 191 in the core region.,

from isolate CAMG27, the clone with SEQ ID NO 173 from the core/E1 region,

from isolate GB438, the clone with SEQ ID NO 177 from the core/ E1 region.

from isolate CAR4/1205, the clone with SEQ ID NO 179 from the core/E1 region,

from isolate CAR1/901, the clone with SEQ ID NO 181 from the core/ E1 region,

from isolate GB809, the clone GB809-4 with SEQ ID NO 189 from the core/E1 region,

clone GB809-2 with SEQ ID NO 169 from the core/E1 region and the clone with SEQ ID NO 163 from the core region,

and from isolate BE100, the clone with SEQ ID NO 155 from the Core/E1 region as shown in Figure 4.

An alignment of these Core/E1 sequences with known Core/E1 sequences is presented in Figure 4. The deduced amino acid sequences with SEQ ID NO 144, 148, 164, 168, 170, 172, 174, 178, 180, 181, 190, 192, 194, 156, 166 are aligned with other prototype sequences in Figure 5. Again, type-specific variation mainly resides in the variable V regions, designated in the present invention, and therefore, type 2d, 3c and type 4-specific amino acids or V regions will be instrumental in diagnosis and therapeutics for HCV type (subtype) 2d, 3c or the different type 4 subtypes.

The NS5b region of isolates NE92, BE98, CAM600, CAMG22, GB438, CAR4/1205, CAR1/501, and BE96 was amplified with primers HCPr206 and HCPr207 (Table 7). The corresponding clones were cloned and sequenced as in example 1 and the corresponding sequences (of which BE98 was partly sequenced) received the following identification numbers:

NE92: SEQ ID NO 145
BE98: SEQ ID NO 149
CAM600: SEQ ID NO 201
CAMG22: SEQ ID NO 203
GB438: SEQ ID NO 207
CAR4/1205: SEQ ID NO 209
CAR1/501: SEQ ID NO 211
BE95: SEQ ID NO 159
BE96: SEQ ID NO 161

An alignment of these NS5b sequences with known NS5b sequences is presented in Figure 1. The deduced amino acid sequences with SEQ ID NO 146, 150, 202, 204, 206, 208, 210, 212, 160, 162 are aligned with other prototype sequences in Figure 2. Again, subtype-specific variations can be observed, and therefore, type 2d, 3c and type 4-specific amino acids or V regions will be instrumental in diagnosis and therapeutics for HCV type (subtype) 2d, 3c or the different type 4 subtypes.

Example 11 : Genotype-specific reactivity of anti-E1 antibodies (Serotyping)

E1 proteins were expressed from vaccinia virus constructs containing a core/E1 region extending from nucleotide positions 355 to 978 (Core/E1 clones described in previous examples including the primers HCPr52 and HCPr54), and expressed proteins from L119 (after the initiator methionine) to W326 of the HCV polyprotein. The expressed protein was modified upon expression in the appropriate host cells (e.g. HeLa, RK13, HuTK-, HepG2) by cleavage between amino acids 191 and 192 of the HCV polyprotein and by the addition of high-mannose type carbohydrate motifs. Therefore, a 30 to 32 kDa glycoprotein could be observed on western blot by means of detection with serum from patients with hepatitis C.

As a reference, a genotype 1b clone obtained from the isolate HCV-B was also expressed in an identical way as described above, and was expressed from recombinant vaccinia virus vvHCV-11A.

A panel of 104 genotyped sera was first tested for reactivity with a cell lysate containing type 1b protein expressed from the recombinant vaccinia virus vvHCV-11A, and compared with cell lysate of RK13 cells infected with a wild type vaccinia virus ('E1/WT'). The lysates were coated as a 1/20 dilution on a normal ELISA microtiter plate (Nunc maxisorb) and left to react with a 1/20 dilution of the respective sera. The panel consisted of 14 type 1a, 38 type 1b, 21 type 2, 21 type 3a, and 9 type 4 sera. Human antibodies were subsequently detected by a goat anti-human IgG conjugated with peroxidase and the enzyme activity was detected. The optical density values of the E1 and wild type lysates were divided and a factor 2 was taken as the cut-off. The results are given in the table A. Eleven out of 14 type 1a sera (79%), 25 out of 38 type 1b sera (66%), 6 out of 21 (29%), 5 out of 21 (24%), and none of the 9 type 4 or the type 5 serum reacted (0%). These experiments clearly show the high prevalence of anti-E1 antibodies reactive with the type 1 E1 protein in patients infected with type 1 (36/52 (69%)) (either type 1a or type 1b), but the low prevalence or absence in non-type 1 sera (11/52 (21%)).

TABLE A

serum	E1/WT
type 1a	
3748	3.15
3807	3.51
5282	1.99
9321	3.12
9324	2.76
9325	6.12
9326	10.56
9356	1.79
9388	3.5
8366	10.72
8380	2.27
10925	4.02
10936	5.04
10938	1.36

type 1b	
5205	2.25
5222	1.33
5246	1.24
5250	13.58
5493	0.87
5573	1.75
8243	1.77
8244	2.05
8316	1.21
8358	5.04
9337	14.47
9410	5
9413	5.51
10905	1.26
10919	5.00
10928	8.72
10929	8.26
10931	2.3
10932	4.41
44	2.37
45	3.14
46	4.37
47	5.68
48	2.97
49	1.18
50	9.85
51	4.51
52	1.11
53	5.20
54	0.98
55	1.48
56	1.06
57	3.85
58	7.6
59	3.28
60	3.23
61	7.82
62	1.92

type 2	
23	0.91
24	1.16
25	2.51
26	0.96
27	1.20
28	0.96
29	2.58
30	8.05
31	0.92
32	0.82
33	5.75
34	0.79
35	0.86
36	0.85
37	0.76
38	0.92
39	1.08
40	2.33
41	2.83
42	1.21
43	0.91
type 3	
1	6.88
2	1.47
3	3.06
4	6.52
5	10.24
6	2.72
7	1.11
8	1.54
9	1.60
10	1.21
11	1.07
12	1.00
13	0.85
14	0.96
15	0.51
16	1.00
17	1.09
18	0.99
19	1.04
20	1.04
21	0.96

type 4	
22	0.87
GB48	0.49
GB113	0.68
GB116	0.73
GB215	0.52
GB358	0.56
GB359	0.71
GB438	1.08
GB516	1.04
type 5	
BE95	0.86

Core/E1 clones of isolates BR36 (type 3a) and BE95 (type 5a) were subsequently recombined into the viruses vvHCV-62 and vvHCV-63, respectively. A genotyped panel of sera was subsequently tested onto cell lysates obtained from RK13 cells infected with the recombinant viruses vvHCV-62 and vvHCV-63. Tests were carried out as described above and the results are given in the table given below (TABLE B). From these results, it can clearly be seen that, although some cross-reactivity occurs (especially between type 1 and 3), the obtained values of a given serum are usually higher on its homologous E1 protein than on an E1 protein of another genotype. For type 5 sera, none of the 5 sera were reactive on type 1 or 3 E1 proteins, while 3 out of 5 were shown to contain anti-E1 antibodies when tested on their homologous type 5 protein. Therefore, in this simple test system, a considerable number of sera can already be serotyped. Combined with the reactivity to type-specific NS4 epitopes or epitopes derived from other type-specific parts of the HCV polyprotein, a serotyping assay may be developed for discriminating the major types of HCV. To overcome the problem of cross-reactivity, the position of cross-reactive epitopes may be determined by someone skilled in the art (e.g. by means of competition of the reactivity with synthetic peptides), and the epitopes evoking cross-reactivity may be left out of the composition to be included in the serotyping assay or may be included in sample diluent to outcompete cross-reactive antibodies.

TABLE B

serum	E1 ^{1b} /WT	E1 ^{3a} /WT	E1 ^{5a} /WT
type 1b			
8316	0.89	0.59	0.80
8358	2.22	2.65	1.96
9337	1.59	0.96	0.93
9410	16.32	9.60	3.62
9413	9.89	2.91	2.85
10905	1.04	0.96	1.05
10919	3.17	2.56	2.96
10928	4.39	2.28	2.07
10929	2.95	2.07	2.08
10931	3.11	1.49	2.11
5	0.86	0.86	0.96
6	3.48	1.32	1.32
7	6.76	4.00	3.77
8	10.88	3.44	4.04
9	1.76	1.88	1.58
10	9.88	7.48	7.20
11	8.48	8.99	8.45
12	0.76	0.72	0.76
13	5.04	5.67	5.37
14	10.48	10.54	11.22
15	5.18	1.62	1.65
type 3			
8332	3.39	4.22	0.66
10907	3.24	4.39	0.96
10908	0.99	0.94	0.98
10934	0.86	0.90	0.90
10927	2.58	2.71	2.44
8210	0.82	0.80	0.86
8344	1.09	6.66	1.17
8351	1.21	1.29	1.22
30	0.85	4.11	0.98
32	0.85	2.16	1.04
type 5			
BE110	0.78	0.95	1.54
BE95	0.79	1.01	4.95
BE111	0.47	0.52	0.65
BE112	0.71	0.75	8.33
BE113	1.01	1.27	2.37
	1.11	1.35	1.60

Table 5. Homologies of new HCV sequences with other known HCV types

Region (nucleotides)	Isolate (type)	1a HCV-1	1b HCV-J	2a HC-J6	2b HC-J8	3a T1	3b T7 T9 T10
Core (1-573)	PC (5)	83.8 (91.6)	84.8 (92.1)	82.6 (90.1)	82.4 (89.0)		
E1 (574-957)	HD10 (3)	61.5 (68.0)	64.6 (68.8)	57.8 (55.5)	56.3 (59.4)		
	BR36 (3)	62.0 (66.4)	62.5 (67.2)	56.5 (53.9)	55.2 (58.6)		
	BR33 (3)	60.7 (67.2)	63.3 (68.0)	56.5 (54.7)	56.0 (58.6)		
	PC (5)	61.4 (64.0)	62.4 (64.8)	54.1 (49.6)	53.3 (47.2)		
	GB358 (4a)	62.5 (69.1)	62.8 (65.9)	59.4 (54.0)	54.4 (54.0)		
	GB549 (4b)	66.0 (72.2)	62.8 (69.8)	59.1 (56.4)	56.5 (54.0)		
	GB809 (4c)	63.3 (69.1)	60.7 (64.3)	56.7 (53.2)	53.0 (51.6)		
NS3 (3856-4209)	PC (5)	74.7 (89)	76.1 (86.4)	76.1 (89.8)	78.0 (89.0)		
NS4 (4892-5292)	BR36 (3)	67.8 (78.5)	69.8 (75.1)	62.0 (67.5)	61.7 (66.0)		
	HD 10 (3)	69.8 (74.6)	66.6 (69.7)	57.8 (59.9)	59.1 (59.9)		
NS4 (4936-5292)	PC (5)	61.3 (62.2)	63.0 (65.5)	52.9 (46.2)	54.3 (43.7)		
NS5b (8023-8235)	BR34 (3)	65.7	66.7	63.9	64.3	94.8 93.9	75.6 77.0
	BR36 (3)	64.3	67.6	64.8	66.7	94.8 93.4	75.1 76.5
	BR33 (3)	65.7	67.1	64.3	64.8	94.8 93.9	76.0 77.5
	GB358 (4a)	67.7 (76.1)	65.6 (77.0)	66.5 (70.8)	65.6 (71.7)		
	GB549 (4b)	68.8 (76.1)	67.1 (77.0)	65.9 (71.7)	65.9 (74.4)		
	GB809 (4c)	68.5 (73.5)	65.0 (73.5)	67.7 (69.9)	67.7 (73.5)		

Shown are the nucleotide homologies (the amino-acid homology is given between brackets) for the region indicated in the left column

Table 6. NS4 sequences of the different genotypes

prototype	TYPE	SYNTHETIC PEPTIDE NS4-1 (NS4a)	SYNTHETIC PEPTIDE NS4-5 (NS4b)	SYNTHETIC PEPTIDE NS4-7 (NS4b)
position->		1 1 6 7 9 0 0 0	1 1 7 - 2 3 0 0	1 1 7 7 3 4 0 0
HCV-1	1a	<u>LSG KPAIIPDREV</u> LYREFDE	SQ <u>HL</u> PYIEQ <u>GMML</u> AEQFKQ R	<u>LAEQFKQ</u> <u>KALGLLQTAS</u> RQA
HCV-1	1b	<u>LSG RPAVIPDREV</u> LYQEFDE	A <u>SH</u> LPYIEQ <u>GMQL</u> AEQFKQ R	<u>LAEQFKQ</u> <u>KALGLLQTAT</u> KQA
HC-J6	2a	<u>VNQ RAVVAPDKEV</u> LYEAfDE	A <u>SR</u> A <u>ALIEE</u> G <u>ORIAE</u> M <u>LKS</u> R	<u>LAEM</u> L <u>KS</u> <u>KIQGLLQQAS</u> KQA
HC-J8	2b	<u>LND RVVVAPDREI</u> LYEAfDE	A <u>SKA</u> A <u>ALIEE</u> G <u>ORMA</u> E <u>MILKS</u> R	<u>MAEM</u> L <u>KS</u> <u>KIQGLLQQAT</u> RQA
BR36	3a	<u>LGK KPAIIPDKEV</u> LYQQ YDE	S <u>QAA</u> PYIEQ <u>AQVIA</u> H <u>QFKR</u> E R	<u>IAHQFKR</u> K <u>VLGLLQRAT</u> QQQ
PC	5	<u>LSG KPAIIPDREA</u> V LYQQ FDE	<u>AASLPYMDE</u> <u>TRAIAGQFKR</u> E R	<u>IAQFKR</u> K <u>VLGFISTIC</u> QKA

, residues conserved in every genotype. Underlined amino acids are type-specific, amino acids in italics are unique to type 3 and 5 sequences

Table 7

SEQ ID NO	Primer NO (polarity)	Sequence from 5' to 3'
63	HCPr161(-)	5'-ACCGGAGGCCAGGAGAGTGATCTCCTCC-3'
64	HCPr162(-)	5'-GGGCTGCTCTATCCTCATCGACGCCATC-3'
65	HCPr163(+)	5'-GCCAGAGGCTCGGAAGGCGATCAGCGCT-3'
66	HCPr164(-)	5'-GAGCTGCTCTGTCTCCTCGACGCCGCA-3'
67	HCPr23(+)	5'-CTCATGGGGTACATTCCGCT-3'
68	HCPr54(-)	5'-CTATTACCACTTCATCATCATATCCCA-3'
69	HCPr116(-)	5'-tttAAATACATCATGRCITGYATG-3'
70	HCPr66(-)	5'-ctattaTTGTATCCCCTGATGAARTTCCACAT-3'
71	HCPr118(-)	5'-actagtcgactaYTGIATICRCTIATRWARTTCCACAT-3'
72	HCPr117(-)	5'-tttAAATACATCGCIRCITGCATGCA-3'
73	HCPr119(-)	5'-actagtcgactaRTTIGCIATIAGCCKRTTCATCCAYTG-3'
74	HCPr131(+)	5'-ggaaattctagaCCITCITGGAYGARAYITGGAARTG-3'
75	HCPr130(-)	5'-ggaaattctagACIGCITAYCARGCIACIGTITGYGC-3'
76	HCPr134(+)	5'-CATATAGATGCCCACTTCCTATC-3'
77	HCPr3(-)	5'-GTGTGCCAGGACCATC-3'
78	HCPr4(-)	5'-GACATGCATGTCATGATGTA-3'
79	HCPr152(+)	5'-TACGCCTCTTCTATATCGGTTGGGCCTG-3'
80	HCPr52(-)	5'-atgTTGGGTAAGGTATCGATAACCCT-3'
81	HCPr41(-)	5'-CCCGGGAGGTCTCGTAGACCGTGCA-3'
82	HCPr40(-)	5'-ctattaAAGATAGAGAAAGAGCAACCGGG-3'
124	HCPR206	5'-tggggatccgttatgatacccgctgcttga-3'
125	HCPR207	5'-ggcgaaattccgttatgatacccgcttggtaaa-3'
141	HCPR109	5'-tgggatatgatgatgaaactggtc-3'
142	HCPR14	5'-ccaggtacaaccgaaccaattgcc-3'

Table 8 : NS4 SEROTYPING

serum	Type 1 NS4			Type 2 NS4			Type 3 NS4		
	1	5	7	1	5	7	1	5	7
type 1a									
101	3	3	3	-	3	-	+/-	-	3
102	1	+/-	2	-	2	-	-	-	1
103	1	3	3	-	+/-	3	-	+/-	3
104	3	3	3	2	2	3	+/-	2	2
105	3	3	3	-	2	2	+/-	+/-	+/-
106	3	1	1	-	1	2	+/-	+/-	-
107	3	3	3	-	2	2	+/-	1	2
108	3	3	3	-	+/-	2	-	-	3
109	3	3	3	-	+/-	2	1	-	-
110	3	3	3	-	+/-	-	-	-	3

serum	Type 1 NS4			Type 2 NS4			Type 3 NS4		
	1	5	7	1	5	7	1	5	7
type 1b									
111	+/-	-	-	-	-	-	-	-	-
112	-	2	3	-	2	1	-	3	3
113	2	3	3	-	1	2	-	3	3
114	2	3	3	-	+	3	-	3	3
115	3	3	3	-	+	1	-	1	1
116	3	3	3	-	+	1	-	-	-
117	3	-	-	3	+/-	+/-	-	-	-
118	1	2	3	-	+/-	2	-	3	3
119	+/-	2	2	+/-	+/-	2	+	1	2
120	-	3	3	-	3	+/-	-	-	-
121	3	3	3	-	+/-	2	2	2	3
122	3	3	1	-	1	2	2	1	1
123	3	3	2	-	1	2	-	1	2
124	3	3	3	-	+/-	2	-	-	-

serum	Type 1 NS4			Type 2 NS4			Type 3 NS4		
	1	5	7	1	5	7	1	5	7
125	3	3	3	1	1	3	2	1	3
126	1	2	2	1	1	1	1	1	1
127	3	2	+/-	-	+/-	1	+/-	+/-	+/-
128	3	3	3	-	+/-	1	2	+/-	+/-
129	2	3	3	-	-	3	-	-	3
130	-	2	1	+/-	-	-	-	-	+/-
131	-	1	1	-	-	-	-	-	-
132	-	-	-	+/-	-	-	+/-	-	-
133	3	3	3	-	-	1	3	1	3
134	-	2	2	-	-	-	-	-	-
135	3	3	3	1	+	2	2	1	3
136	-	3	3	+/-	+/-	+/-	+/-	-	3
137	+/-	+/-	+/-	+/-	+/-	2	+/-	-	-
138	3	3	3	+/-	+/-	2	1	1	3
type 2a									
139	3	-	-	3	3	+/-	1	-	-
140	+/-	-	-	3	3	+/-	3	-	-
141	2	-	-	2	1	+/-	2	-	-
142	-	-	-	-	-	-	-	-	-
143	-	+/-	+/-	+/-	1	2	1	+/-	+/-
144	1	1	+	+	1	3	2	1	2
145	-	+/-	+/-	+/-	3	1	2	+/-	+/-
146	-	-	-	+/-	3	1	-	-	-
147	-	+/-	+/-	+/-	-	-	+/-	-	-
148	-	-	-	-	-	-	-	-	-

SUBSTITUTE SHEET (RULE 26)

serum	Type 1 NS4			Type 2 NS4			Type 3 NS4		
	1	5	7	1	5	7	1	5	7
type 2b	-	+/-	+/-	-	-	-	-	-	-
149	-	+/-	+/-	3	3	1	2	+/-	+/-
type 3	+/-	+/-	+/-	+/-	+/-	+/-	1	3	3
150	-	-	-	-	-	-	2	-	2
151	+/-	-	-	-	-	-	3	-	-
152	-	-	-	-	-	-	-	-	-
153	-	-	-	-	-	-	-	-	-
154	+/-	1	3	-	-	-	2	1	3
155	-	2	3	-	-	-	-	-	-
156	-	-	-	-	-	-	-	-	-
157	-	-	-	-	-	-	+/-	2	2
158	2	-	-	-	-	-	1	2	2
159	-	-	-	-	-	-	+/-	-	3
160	-	-	-	-	-	-	+/-	2	3
161	-	-	-	-	-	-	+/-	3	2
type 4	-	-	-	-	-	-	-	-	-
162	1	-	-	-	-	-	-	-	-
163	2	-	-	+/-	+/-	+/-	-	-	-

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CLAIMS

1 A composition comprising or consisting of at least one polynucleic acid containing 8 or more contiguous nucleotides selected from at least one of the following HCV sequences.

- an HCV type 3 genomic sequence, more particularly in any of the following regions:
 - the region spanning positions 417 to 957 of the Core/E1 region of HCV subtype 3a,
 - the region spanning positions 4664 to 4730 of the NS3 region of HCV type 3,
 - the region spanning positions 4892 to 5292 of the NS3/4 region of HCV type 3,
 - the region spanning positions 8023 to 8235 of the NS5 region of HCV subtype 3a,
 - an HCV subtype 3c genomic sequence,
- an HCV subtype 2d genomic sequence,
- an HCV type 4 genomic sequence,
- the coding region of HCV subtype 5a,

with said nucleotide numbering being with respect to the numbering of HCV nucleic acids as shown in Table 1, and with said polynucleic acids containing at least one nucleotide difference with known HCV polynucleic acid sequences in the above-indicated regions, or the complement thereof

2. A composition according to claim 1, wherein said polynucleic acids correspond to a nucleotide sequence selected from any of the following HCV genomic sequences

- an HCV genomic sequence as having a homology of at least 67%, preferably more than 69%, most preferably 71% or more to any of the sequences as represented in SEQ ID NO 13, 15, 17, 19, 21, 23, 25 or 27 in the region spanning positions 417 to 957 of the Core/E1 region;
- an HCV genomic sequence as having a homology of at least 65%, preferably more than 67%, most preferably 69% or more to any of the sequences as represented in SEQ ID NO 19, 21, 23, 25 or 27 in the region spanning positions 574 to 957 of the E1 region.
- an HCV genomic sequence, having a homology of at least 79%, more preferably at least 81%, most preferably more than 83% or more to any of the sequences as represented in

SEQ ID NO 147 in the region spanning positions 1 to 378 of the Core region ,

- an HCV genomic sequence having a homology of at least 74%, more preferably at least 76%, most preferably more than 78% or more to any of the sequences as represented in SEQ ID NO 13, 15, 17, 19, 21, 23, 25 or 27 in the region spanning positions 417 to 957 in the Core/E1 region,
- an HCV genomic sequence having a homology of at least 74%, preferably more than 76%, most preferably 78% or more to any of the sequences as represented in SEQ ID NO 13, 15, 17, 19, 21, 23, 25 or 27 in the region spanning positions 574 to 957 in the E1 region,
- an HCV genomic sequence having a homology of more than 73.5%, preferably more than 74%, most preferably 75% homology to any of the sequence as represented in SEQ ID NO 29 in the region spanning positions 4664 to 4730 of the NS3 region,
- an HCV genomic sequence having a homology of more than 70%, preferably more than 72%, most preferably more than 74% homology to any of the sequences as represented in SEQ ID NO 29, 31, 33, 35, 37 or 39 in the region spanning positions 4892 to 5292 in the NS3/NS4 region,
- an HCV genomic sequence having a homology of more than 95%, preferably 95.5%, most preferably 96% homology to any of the sequences as represented in SEQ ID NO 5, 7, 1, 3, 9 or 11 in the region spanning positions 8023 to 8235 of the NS5 region,
- an HCV genomic sequence of the BR36 subgroup of HCV type 3a having a homology of more than 96%, preferably 96.5%, most preferably 97% homology to any of the sequences as represented in SEQ ID NO 5, 7, 1, 3, 9 or 11 in the region spanning positions 8023 to 8192 of the NS5B region,
- an HCV genomic sequence having a homology of more than 79%, more preferably more than 81%, and most preferably more than 83% to the sequence as represented in SEQ ID NO 149 in the region spanning positions 7932 to 8271 in the NS5B region.

3. A composition according to claim 1, wherein said polynucleic acids correspond to a nucleotide sequence selected from any of the following HCV genomic sequences

- an HCV genomic sequence having a homology of more than 85%, preferably more than 86%, most preferably more than 87% homology to any of the sequences as represented in SEQ ID NO 41, 43, 45, 47, 49, 51, 53 or 151 in the region spanning positions 1 to 573 of the Core region,

- an HCV genomic sequence having a homology of more than 61%, preferably more than 63%, most preferably more than 65% homology to any of the sequences as represented in SEQ ID NO 41, 43, 45, 47, 49, 51, 53, 153 or 155 in the region spanning positions 574 to 957 of the E1 region;
- an HCV genomic sequence having a homology of more than 76.5%, preferably of more than 77%, most preferably of more than 78% homology with any of the sequences as represented in SEQ ID NO 55, 57, 197 or 199 in the region spanning positions 3856 to 4209 of the NS3 region;
- an HCV genomic sequence having a homology of more than 68%, preferably of more than 70%, most preferably of more than 72% homology with the sequence as represented in SEQ ID NO 157 in the region spanning positions 980 to 1179 of the E1/E2 region;
- an HCV genomic sequence having a homology of more than 57%, preferably more than 59%, most preferably more than 61% homology to any of the sequences as represented in SEQ ID NO 59 or 61 in the region spanning positions 4936 to 5296 of the NS4 region;
- an HCV genomic sequence having a homology of more than 93%, preferably more than 93.5%, most preferably more than 94% homology to any of the sequences as represented in SEQ ID NO 159 or 161 in the region spanning positions 7932 to 8271 of the NS5B region.

4 A composition according to claim 1, wherein said polynucleic acids correspond to a nucleotide sequence selected from any of the following HCV genomic sequences

- an HCV genomic sequence having a homology of more than 66%, preferably more than 68%, most preferably more than 70% homology in the E1 region spanning positions 574 to 957 to any of the sequences as represented in SEQ ID NO 118, 120 or 122 in the region spanning positions 1 to 957 of the Core/E1 region;
- an HCV genomic sequence having a homology of more than 71%, preferably more than 72%, most preferably more than 74% homology to any of the sequences as represented in SEQ ID NO 118, 120 or 122 in the region spanning positions 379 to 957;
- an HCV genomic sequence having a homology of more than 85%, preferably more than 86%, most preferably more than 86.5% homology to any of the sequences as represented in SEQ ID NO 183, 185 or 187 in the region spanning positions 379 to 957 of the E1 region;
- an HCV genomic sequence having a homology of more than 81%, preferably more than

83%, most preferably more than 85% homology to the sequence as represented in SEQ ID NO 189 in the region spanning positions 379 to 957 of the E1 region,

- an HCV genomic sequence having a homology of more than 85%, preferably more than 87%, most preferably more than 89% homology to any of the sequences as represented in SEQ ID NO 167 or 169 in the region spanning positions 379 to 957 of the E1 region,
- an HCV genomic sequence having a homology of more than 79%, preferably more than 81%, most preferably more than 83% homology to any of the sequences as represented in SEQ ID NO 171 or 173 in the region spanning positions 379 to 957 of the E1 region,
- an HCV genomic sequence having a homology of more than 84%, preferably more than 86%, most preferably more than 88% homology to the sequence as represented in SEQ ID NO 175 in the region spanning positions 379 to 957 of the E1 region,
- an HCV genomic sequence having a homology of more than 83%, preferably more than 85%, most preferably more than 87% homology to the sequence as represented in SEQ ID NO 177 in the region spanning positions 379 to 957 of the E1 region ,
- an HCV genomic sequence having a homology of more than 76%, preferably more than 78%, most preferably more than 80% homology to the sequence as represented in SEQ ID NO 179 in the region spanning positions 379 to 957 of the E1 region.
- an HCV genomic sequence having a homology of more than 84%, preferably more than 86%, most preferably more than 88% homology to the sequence as represented in SEQ ID NO 181 in the region spanning positions 379 to 957 of the E1 region ,
- an HCV genomic sequence having a homology of more than 73%, preferably more than 75%, most preferably more than 77% homology to any of the sequences as represented in SEQ ID NO 106, 108, 110, 112, 114, or 116 in the region spanning positions 7932 to 8271 of the NS5 region ;
- an HCV genomic sequence having a homology of more than 88%, preferably more than 89%, most preferably more than 90% homology to any of the sequences as represented in SEQ ID NO 106, 108, 110, or 112 in the region spanning positions 7932 to 8271 of the NS5 region;
- an HCV genomic sequence having a homology of more than 88%, preferably more than 89%, most preferably more than 90% homology to any of the sequences as represented in SEQ ID NO 116 or 201 in the region spanning positions 7932 to 8271 of the NS5 region,
- an HCV genomic sequence having a homology of more than 87%, preferably more than

- 89%, most preferably more than 90% homology to the sequence as represented in SEQ ID NO 203 in the region spanning positions 7932 to 8271 of the NS5 region;
- an HCV genomic sequence having a homology of more than 85%, preferably more than 87%, most preferably more than 89% homology to the sequence as represented in SEQ ID NO 114 in the region spanning positions 7932 to 8271 of the NS5 region;
 - an HCV genomic sequence having a homology of more than 86%, preferably more than 87%, most preferably more than 88% homology to the sequence as represented in SEQ ID NO 207 in the region spanning positions 7932 to 8271 of the NS5 region;
 - an HCV genomic sequence having a homology of more than 84%, preferably more than 86%, most preferably more than 88% homology to the sequence as represented in SEQ ID NO 209 in the region spanning positions 7932 to 8271 of the NS5 region;
 - an HCV genomic sequence having a homology of more than 81%, preferably more than 83%, most preferably more than 85% homology to the sequence as represented in SEQ ID NO 211 in the region spanning positions 7932 to 8271 of the NS5 region
- 5 A composition according to claim 1, wherein said polynucleic acids correspond to a nucleotide sequence selected from any of the following HCV genomic sequences
- an HCV genomic sequence having a homology of more than 78%, preferably more than 80%, most preferably more than 82% homology to the sequence as represented in SEQ ID NO 143 in the region spanning positions 379 to 957 of the Core/E1 region,
 - an HCV genomic sequence having a homology of more than 74%, preferably more than 76%, most preferably more than 78% homology to the sequence as represented in SEQ ID NO 143 in the region spanning positions 574 to 957,
 - an HCV genomic sequence having a homology of more than 87%, preferably more than 89%, most preferably more than 91% homology to the sequence as represented in SEQ ID NO 145 in the region spanning positions 7932 to 8271 of the NS5B region
- 6 A composition according to any of claims 1 to 5, wherein said polynucleic acid is liable to act as a primer for amplifying the nucleic acid of a certain isolate belonging to the genotype from which the primer is derived
- 7 A composition according to any of claims 1 to 5, wherein said polynucleic acid is able to act as a hybridization probe for specific detection and/or classification into types of a

nucleic acid containing said nucleotide sequence, with said oligonucleotide being possibly labelled or attached to a solid substrate

3 Use of a composition according to any of claims 1 to 7 for *in vitro* detecting the presence of one or more HCV genotypes, more particularly for detecting the presence of a nucleic acid of any of the HCV genotypes having a nucleotide sequence as defined in any of claims 1 to 5, present in a biological sample liable to contain them, comprising at least the following steps:

- (i) possibly extracting sample nucleic acid,
- (ii) possibly amplifying the nucleic acid with at least one of the primers according to claim 6 or any other HCV type 2, HCV type 3, HCV type 4, HCV type 5 or universal HCV primer,
- (iii) hybridizing the nucleic acids of the biological sample, possibly under denatured conditions, and with said nucleic acids being possibly labelled during or after amplification, at appropriate conditions with one or more probes according to claim 7, with said probes being preferably attached to a solid substrate,
- (iv) washing at appropriate conditions,
- (v) detecting the hybrids formed,
- (vi) inferring the presence of one or more HCV genotypes present from the observed hybridization pattern

9 A composition consisting of or comprising at least one peptide or polypeptide containing in its sequence a contiguous sequence of at least 5 amino acids of an HCV polyprotein encoded by any of the polynucleic acids according to any of claims 1 to 5.

10 A composition according to claim 9, wherein said contiguous sequence contains in its sequence at least one of the following amino acid residues:

L7, Q43, M44, S60, R67, Q70, T71, A79, A87, N106, K115, A127, A190, S130, V134, G142, I144, E152, A157, V158, P165, S177 or Y177, I178, V180 or E180 or F182, R184, I186, H187, T189, A190, S191 or G191, Q192 or L192 or I192 or V192 or E192, N193 or H193 or P193, W194 or Y194, H195, A197 or I197 or V197 or T197, V202, L203 or L203, Q208, A210, V212, F214, T216, R217 or D217 or E217 or V217, H218 or N218, H219 or V219 or L219, L227 or I227, M231 or E231 or Q231, T232 or D232 or A232 or K232, Q235

or I₂₃₅, A₂₃₇ or T₂₃₇, I₂₄₂, I₂₄₆, S₂₄₇, S₂₄₈, V₂₄₉, S₂₅₀ or Y₂₅₀, I₂₅₁ or V₂₅₁ or M₂₅₁ or F₂₅₁, D₂₅₂, T₂₅₄ or V₂₅₄, L₂₅₅ or V₂₅₅, E₂₅₆ or A₂₅₆, M₂₅₈ or F₂₅₈ or V₂₅₈, A₂₆₀ or Q₂₆₀ or S₂₆₀, A₂₆₁, T₂₆₄ or Y₂₆₄, M₂₆₅, I₂₆₆ or A₂₆₆, A₂₆₇, G₂₆₈ or T₂₆₈, F₂₇₁ or M₂₇₁ or V₂₇₁, I₂₇₇, M₂₈₀ or H₂₈₀, I₂₈₄ or A₂₈₄ or L₈₄, V₂₇₄, V₂₉₁, N₂₉₂ or S₂₉₂, R₂₉₃ or I₂₉₃ or Y₂₉₃, Q₂₉₄ or R₂₉₄, L₂₉₇ or I₂₉₇ or Q₂₉₇, A₂₉₉ or K₂₉₉ or Q₂₉₉, N₃₀₃ or T₃₀₃, T₃₀₈ or L₃₀₈, T₃₁₀ or F₃₁₀ or A₃₁₀ or D₃₁₀ or V₃₁₀, L₃₁₃, G₃₁₇ or Q₃₁₇, L₃₃₃, S₃₅₁, A₃₅₈, A₃₅₉, A₃₆₃, S₃₆₄, A₃₆₆, T₃₆₉, L₃₇₃, F₃₇₆, Q₃₈₆, I₃₈₇, S₃₉₂, I₃₉₉, F₄₀₂, I₄₀₃, R₄₀₅, D₄₅₄, A₄₆₁, A₄₆₃, T₄₆₄, K₄₈₄, Q₅₀₀, E₅₀₁, S₅₂₁, K₅₂₂, H₅₂₄, N₅₂₈, S₅₃₁, S₅₃₂, V₅₃₄, F₅₃₆, F₅₃₇, M₅₃₉, I₅₄₆, C₁₂₈₂, A₁₂₈₃, H₁₃₁₀, V₁₃₁₂, Q₁₃₂₁, P₁₃₆₈, V₁₃₇₂, V₁₃₇₃, K₁₄₀₅, Q₁₄₀₆, S₁₄₀₉, A₁₄₂₄, A₁₄₂₉, C₁₄₃₅, S₁₄₃₆, S₁₄₅₆, H₁₄₉₆, A₁₅₀₄, D₁₅₁₀, D₁₅₂₉, I₁₅₄₃, N₁₅₆₇, D₁₅₅₆, N₁₅₆₇, M₁₅₇₂, Q₁₅₇₉, L₁₅₈₁, S₁₅₈₃, F₁₅₈₅, V₁₅₉₅, E₁₆₀₆ or T₁₆₀₆, M₁₆₁₁, V₁₆₁₂ or L₁₆₁₂, P₁₆₃₀, C₁₆₃₆, P₁₆₅₁, T₁₆₅₆ or I₁₆₅₆, L₁₆₆₃, V₁₆₆₇, V₁₆₇₇, A₁₆₈₁, H₁₆₈₅, E₁₆₈₇, G₁₆₈₉, V₁₆₉₅, A₁₇₀₀, Q₁₇₀₄, Y₁₇₀₅, A₁₇₁₃, A₁₇₁₄ or S₁₇₁₄, M₁₇₁₈, D₁₇₁₉, A₁₇₂₁ or T₁₇₂₁, R₁₇₂₂, A₁₇₂₃ or V₁₇₂₃, H₁₇₂₆ or G₁₇₂₆, E₁₇₃₀, V₁₇₃₂, F₁₇₃₅, I₁₇₃₆, S₁₇₃₇, R₁₇₃₈, T₁₇₃₉, G₁₇₄₀, Q₁₇₄₁, K₁₇₄₂, Q₁₇₄₃, A₁₇₄₄, T₁₇₄₅, L₁₇₄₆, E₁₇₄₇ or K₁₇₄₇, I₁₇₄₉, A₁₇₅₀, T₁₇₅₁ or A₁₇₅₁, V₁₇₅₃, N₁₇₅₅, K₁₇₅₆, A₁₇₅₇, P₁₇₅₈, A₁₇₅₉, H₁₇₆₂, T₁₇₆₃, Y₁₇₆₄, P₂₆₄₅, A₂₆₄₇, K₂₆₅₀, K₂₆₅₃ or L₂₆₅₃, S₂₆₆₄, N₂₆₇₃, F₂₆₈₀, K₂₆₈₁, L₂₆₈₆, H₂₆₉₂, Q₂₆₉₅ or L₂₆₉₅ or I₂₆₉₅, V₂₇₁₂, F₂₇₁₅, V₂₇₁₉ or Q₂₇₁₉, T₂₇₂₂, T₂₇₂₄, S₂₇₂₅, R₂₇₂₆, G₂₇₂₉, Y₂₇₃₅, H₂₇₃₉, I₂₇₄₈, G₂₇₄₆ or I₂₇₄₆, I₂₇₄₈, P₂₇₅₂ or K₂₇₅₂, P₂₇₅₄ or T₂₇₅₄, T₂₇₅₇ or P₂₇₅₇,

with said notation being composed of a letter representing the amino acid residue by its one-letter code, and a number representing the amino acid numbering according to Kato et al., 1990 as shown in Table 1

11 A composition according to any of claims 9 or 10, wherein said contiguous sequence is selected from any of the following HCV amino acid sequences

- a sequence having a homology of more than 72%, preferably more than 74%, and most preferably more than 77% homology to any of the amino acid sequences as represented in SEQ ID NO 14, 16, 18, 20, 22, 24, 26 or 28 in the region spanning positions 140 to 319 in the Core/E1 region,
- a sequence having a homology of more than 70%, preferably more than 72%, and most preferably more than 75% homology to any of the amino acid sequences as represented in SEQ ID NO 14, 16, 18, 20, 22, 24, 26 or 28 in the E1 region spanning positions 192 to

319,

- a sequence having a homology of more than 86%, preferably more than 88%, and most preferably more than 90% homology to the amino acid sequences as represented in SEQ ID NO 148 in the region spanning positions 1 to 110 in the Core region,
- a sequence having a homology of more than 76%, preferably more than 78%, most preferably more than 80% to any of the amino acid sequences as represented in SEQ ID NO 30, 32, 34, 36, 38 or 40 in the region spanning positions 1646 to 1764 in the NS3/NS4 region,
- a sequence having a homology of more than 81.5%, preferably more than 83%, and most preferably more than 86% homology to any of the amino acid sequences as represented in SEQ ID NO 14, 16, 18, 20, 22, 24, 26 or 28 in the E1 region spanning positions 192 to 319,
- a sequence having a homology of more than 86%, preferably more than 88%, most preferably more than 90% to the amino acid sequence as represented in SEQ ID NO 150 in the region spanning positions 2645 to 2757 in the NS5B region,

12. A composition according to any of claims 9 or 10, wherein said contiguous sequence is selected from any of the following HCV amino acid sequences:

- a sequence having a homology of more than 80%, preferably more than 82%, most preferably more than 84% homology to any of the amino acid sequences as represented in SEQ ID NO 118, 120, and 122 in the region spanning positions 127 to 319,
- a sequence having a homology of more than 73%, preferably more than 75%, most preferably more than 78% homology in the E1 region spanning positions 192 to 319 to any of the amino acid sequences as represented in SEQ ID NO 118, 120, and 122, in the region spanning positions 127 to 319,
- a sequence having more than 85%, preferably more than 86%, most preferably more than 87% homology to any of the amino acid sequences as represented in SEQ ID NO 118, 120 or 122, in the region spanning positions 192 to 319

13. A composition according to any of claims 9 or 10, wherein said contiguous sequence is selected from any of the following HCV amino acid sequences

- a sequence having more than 93%, preferably more than 94%, most preferably more than 95% homology in the region spanning Core positions 1 to 191 to any of the amino acid

- sequences as represented in SEQ ID NO 42, 44, 46, 48, 50, 52, 54, or 152;
- a sequence having more than 73%, preferably more than 74%, most preferably more than 76% homology in the region spanning E1 positions 192 to 319 to any of the amino acid sequences as represented in SEQ ID NO 42, 44, 46, 48, 50, 52, 54, 154 or 156;
 - a sequence spanning positions 1286 to 1403 of the NS3 region, with said sequence being characterized as having more than 90%, preferably more than 91%, most preferably more than 92% homology to any of the amino acid sequences represented in SEQ ID NO 56 to 58;
 - a sequence spanning positions 1646 to 1764 of the NS3/4 region, with said sequence being characterized as having more than 66%, more particularly 68%, most particularly 70% or more homology to any of the amino acid sequences as represented in SEQ ID NO 60 or 62

14. A composition according to any of claims 9 to 10, wherein said contiguous sequence is selected from any of the following HCV amino acid sequences

- a sequence having a more than 83%, preferably more than 85%, most preferably more than 87% homology in the region spanning Core positions 1 to 319 to the amino acid sequence as represented in SEQ ID NO 144,
- a sequence having a more than 79%, preferably more than 81%, most preferably more than 84% homology in the region spanning E1 positions 192 to 319 to the amino acid sequence as represented in SEQ ID NO 144;
- a sequence having more than 95%, more particularly 96%, most particularly 97% or more homology to the amino acid sequence as represented in SEQ ID NO 146, in the region spanning positions 2645 to 2757 of the NS5B region

15. A composition according to any of claims 9 to 14, wherein said sequence is selected from the following peptides:

QPTGRSWGQ (SEQ ID NO 93)
RSEGRTSWAQ (SEQ ID NO 220)
RTEGRTSWAQ (SEQ ID NO 221)
SRRQPIPRARRTEGRSWAQ (SEQ ID NO 268)
LEWRNTSGLYVL (SEQ ID NO 83)
VNYRNASGIYHI (SEQ ID NO 126)

QHYRNISGIYHV (SEQ ID NO 127)
EHYRNASGIYHI (SEQ ID NO 128)
IHYRNASGIYHI (SEQ ID NO 224)
VPYRNASGIYHV (SEQ ID NO 84)
VNYRNASGIYHI (SEQ ID NO 225)
VNYRNASGVYHI (SEQ ID NO 226)
VNYHNTSGIYHL (SEQ ID NO 227)
QHYRNASGIYHV (SEQ ID NO 228)
QHYRNVSGIYHV (SEQ ID NO 229)
IHYRNASDGGYI (SEQ ID NO 230)
LQVKNTSSSYMV (SEQ ID NO 231)
VYEADDVILHT (SEQ ID NO 85)
VYETEHHLHL (SEQ ID NO 129)
VYEADHHIMHL (SEQ ID NO 130)
VYETDHHLHL (SEQ ID NO 131)
VYEADNLILHA (SEQ ID NO 86)
VWQLRAIVLV (SEQ ID NO 232)
VYEADYHILHL (SEQ ID NO 233)
VYETDNHILHL (SEQ ID NO 234)
VYETENHILHL (SEQ ID NO 235)
VFETVHHILHL (SEQ ID NO 236)
VFETEHHLHL (SEQ ID NO 237)
VFETDHIMHL (SEQ ID NO 238)
VYETENHILHL (SEQ ID NO 239)
VYEADALILHA (SEQ ID NO 240)
VQDGNTSTCWTPV (SEQ ID NO 87)
VQDGNTSACWTPV (SEQ ID NO 241)
VRVGNQSRCWVAL (SEQ ID NO 132)
VRTGNTSRCWVPL (SEQ ID NO 133)
VRAGNVSRCWTPV (SEQ ID NO 134)
EEKGNISRCWIPV (SEQ ID NO 242)
VKTGNQSRCWVAL (SEQ ID NO 243)
VRTGNQSRCWVAL (SEQ ID NO 244)

VKTGNQSRCWIAL (SEQ ID NO 245)
VKTGNVSR CWIPL (SEQ ID NO 247)
VKTGNVSR CWISL (SEQ ID NO 248)
VRKD NVSRCWVQI (SEQ ID NO 249)
VRYVGATTAS (SEQ ID NO 89)
APYIGAPLES (SEQ ID NO 135)
APYVGAPLES (SEQ ID NO 136)
AVSMIDAPLES (SEQ ID NO 137)
APSLGAVTAP (SEQ ID NO 90)
APSFGAVTAP (SEQ ID NO 250)
VSQPGALT KG (SEQ ID NO 251)
VKYVGATTAS (SEQ ID NO 252)
APYIGAPVES (SEQ ID NO 253)
AQHLNAPLES (SEQ ID NO 254)
SPYVGAPLEP (SEQ ID NO 255)
SPYAGAPLEP (SEQ ID NO 256)
APYLGAPLEP (SEQ ID NO 257)
APYLGAPLES (SEQ ID NO 258)
APYVGAPLES (SEQ ID NO 259)
VPYLGAPLTS (SEQ ID NO 260)
APHLRAPLSS (SEQ ID NO 261)
APYLGAPLTS (SEQ ID NO 262)
RPRRHQTVQT (SEQ ID NO 91)
QPRRHWT TQD (SEQ ID NO 138)
RPRRHWT TQD (SEQ ID NO 139)
RPRQHATVQN (SEQ ID NO 92)
RPRQHATVQD (SEQ ID NO 263)
SPQHIIKFVQD (SEQ ID NO 264)
RPRRLWTTQE (SEQ ID NO 265)
PPRIHETTQD (SEQ ID NO 266)
TISYANGSGPSDDK (SEQ ID NO 267)

16 Recombinant vector, particularly for cloning and/or expression, with said recombinant

vector comprising a vector sequence, an appropriate prokaryotic, eukaryotic or viral promoter sequence followed by the nucleotide sequences as defined in claims 1 to 5, with said recombinant vector allowing the expression of any one of the HCV type 2 and/or HCV type 3 and/or type 4 and/or type 5 derived polypeptides according to any of claims 9 to 15 in a prokaryotic, or eukaryotic host, or in living mammals when injected as naked DNA, and more particularly a recombinant vector allowing the expression of any of the following HCV type 2, HCV type 3, type 4 or type 5 polypeptides spanning the following amino acid positions

- a polypeptide starting at position 1 and ending at any position in the region between positions 70 and 326, more particularly a polypeptide spanning positions 1 to 70, 1 to 85, positions 1 to 120, positions 1 to 150, positions 1 to 191, positions 1 to 200, for expression of the Core protein, and positions 1 to 263, positions 1 to 326, for expression of the Core and E1 protein,
- a polypeptide starting at any position in the region between positions 117 and 192, and ending at any position in the region between positions 263 and 326, more particularly from positions 119 to 326, for expression of E1, or forms that have the putative membrane anchor deleted (positions 264 to 293 plus or minus 8 amino acids);
- a polypeptide starting at any position in the region between positions 1556 and 1638, and ending at any position in the region between positions 1739 and 1764, for expression of the NS4 regions, more particularly a polypeptide starting at position 1658 and ending at position 1711 for expression of the NS4a antigen, and more particularly, a polypeptide starting at position 1712 and ending between positions 1743 and 1972, for example 1712-1743, 1712-1764, 1712-1782, 1712-1972, 1712 to 1782 and 1902 to 1972 for expression of the NS4b protein or parts thereof.

17. A composition according to any of claims 9 to 15, wherein said polypeptide is a recombinant polypeptide expressed by means of an expression vector as defined in claim 16

18. A composition according to any of claims 9 to 15 or 16, for use in a method for immunizing a mammal, preferably humans, against HCV comprising administrating a sufficient amount of the composition possibly accompanied by pharmaceutically acceptable adjuvants, to produce an immune response, more particularly a vaccine composition including HCV type 3 polypeptides derived from the E1, Core, or NS4 region and/or type 4 and/or type 5 and/or type 2 polypeptides

19 Antibody raised upon immunization with a composition according to any of claims 9 to 15, 17 or 18, by means of a process according to claim 18, with said antibody being reactive with any of the polypeptides as defined in any of claims 9 to 15, 17 or 18

20 Process for detecting *in vitro* HCV present in biological sample liable to contain it, comprising at least the following steps:

- (i) contacting the biological sample to be analyzed for the presence of HCV antibodies with any of the compositions according to claims 9 to 15, 17 or 18, preferentially in an immobilized form under appropriate conditions which allow the formation of an immune complex, wherein said polypeptide is preferentially in the form of a biotinylated polypeptide and is covalently bound to a solid substrate by means of streptavidin or avidin complexes,
- (ii) removing unbound components,
- (iii) incubating the immune complexes formed with heterologous antibodies, which specifically bind to the antibodies present in the sample to be analyzed, with said heterologous antibodies having conjugated to a detectable label under appropriate conditions,
- (iv) detecting the presence of said immune complexes visually or by means of densitometry and inferring the HCV serotype(s) present from the observed hybridization pattern.

21. Use of a composition according to any of claims 9 to 15, 17 or 18, for incorporation into a serotyping assay for detecting one or more serological types of HCV present in a biological sample liable to contain it, more particularly for detecting E1 and NS4 antigens or antibodies of the different types to be detected combined in one assay format, comprising at least the following steps.

- (i) contacting the biological sample to be analyzed for the presence of HCV antibodies or antigens of one or more serological types, with at least one of the compositions according to claims 9 to 15, 17 or 18 in an immobilized form under appropriate conditions which allow the formation of an immune complex, (wherein said polypeptide is preferentially in the form of a biotinylated polypeptide and is covalently bound to a solid substrate by means of streptavidin or avidin complexes),

- (ii) removing unbound components,
- (iii) incubating the immune complexes formed with heterologous antibodies, which specifically bind to the antibodies present in the sample to be analyzed, with said heterologous antibodies having conjugated to a detectable label under appropriate conditions.
- (iv) detecting the presence of said immune complexes visually or by means of densitometry and inferring the HCV serological types present from the observed binding pattern

22 A kit for determining the presence of HCV genotypes as defined in any of claims 1 to 5 present in a biological sample liable to contain them, comprising

- possibly at least one primer composition containing any primer selected from those defined in claim 6 or any other HCV type 2 and/or HCV type 3 and/or HCV type 4 and/or HCV type 5, or universal HCV primers,
- at least one probe composition according to claim 7, preferably in combination with other polypeptides or peptides from HCV type 1, type 2 or other types of HCV, with said probes being preferentially immobilized on a solid substrate, and more preferentially on one and the same membrane strip,
- a buffer or components necessary for producing the buffer enabling hybridization reaction between these probes and the possibly amplified products to be carried out,
- a means for detecting the hybrids resulting from the preceding hybridization,
- possibly also including an automated scanning and interpretation device for inferring the HCV genotype(s) present in the sample from the observed hybridization pattern

23 A kit for determining the presence of HCV antibodies according to any of claims 9 to 15, 17 or 18 present in a biological sample liable to contain them, comprising

- at least one polypeptide composition according to any of claims 9 to 15, 17 or 18, with said polypeptides being preferentially immobilized on a solid substrate, and more preferentially on one and the same membrane strip,
- a buffer or components necessary for producing the buffer enabling binding reaction between these polypeptides and the antibodies against HCV present in the biological sample,
- a means for detecting the immune complexes formed in the preceding binding

reaction,

- possibly also including an automated scanning and interpretation device for inferring the HCV genotype present in the sample from the observed binding pattern.

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INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁵ : C12N 15/51, C12Q 1/68, A61K 39/29, G01N 33/576, C07N 14/18, C12Q 1/70, C07K 16/10		A2	(11) International Publication Number: WO 94/25601 (43) International Publication Date: 10 November 1994 (10.11.94)
(21) International Application Number: PCT/EP94/01323 (22) International Filing Date: 27 April 1994 (27.04.94)		(81) Designated States: AT, AU, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, ES, FI, GB, GE, HU, JP, KG, KP, KR, KZ, LK, LU, LV, MD, MG, MN, MW, NL, NO, NZ, PT, RO, RU, SD, SE, SL, SK, TI, TT, UA, US, UZ, VN, European patent (AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG).	
(30) Priority Data: 93401099.2 27 April 1993 (27.04.93) (34) Countries for which the regional or international application was filed: GB et al. 93402019.9 5 August 1993 (05.08.93) (34) Countries for which the regional or international application was filed: EP GB et al.		Published Without international search report and to be republished upon receipt of that report.	
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(54) Title: NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES AND THEIR USE AS THERAPEUTIC AND DIAGNOSTIC AGENTS

(57) Abstract

The present invention relates to a polynucleic acid composition comprising or consisting of at least one polynucleic acid containing 8 or more contiguous nucleotides corresponding to a nucleotide sequence from the region spanning positions 417 to 957 of the Core/EI region of HCV type 3; and/or the region spanning positions 4664 to 4730 of the NS3 region of HCV type 3; and/or the region spanning positions 4892 to 5292 of the NS3/4 region of HCV type 3; and/or the region spanning positions 8 023 to 8 235 of the NS5 region of the BR36 subgroup of HCV type 3a; and/or the coding region of HCV type 4 starting at nucleotide 379 in the core region; and/or the coding region of HCV type 4; and/or the coding region of HCV type 5, with said nucleotide numbering being with respect to the numbering of HCV nucleic acids as shown in Table 1, and with said polynucleic acids containing at least one nucleotide difference with known HCV type 1, and/or HCV type 2 genomes in the above-indicated regions, or the complement thereof.

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Figure 1

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Figure 1 - Continued 1

GB4 8	4C	7932	G-
GB1 16	4C		AGG--
GB2 15	4C		-T--
GB3 58	4C		-G-
GB8 09	4e		A-GGTC--
CAM600	4e		-A-GGTC--
CAMG22	4f		-A-GGTC--
GB5 49	4g		-A-GGTC--
GB4 38	4h		-A-GGTC--
CAR4/1205	4i		-A-GGTC--
CAR1/501	4j		-A-GGTC--
EG-13	4k		-A-GGTC--
EG-19	4k		-A-GGTC--
BE95	5a		-AATG-C-A-T-C-T-
BE96	5a		-ATTG-T-A-T-C-A-
CHR18	5a		-AATG-T-A-T-T-T-
CHR19	5a		-AATG-T-A-T-C-T-
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Figure 1 - Continued 2

	SEQ ID	7982	8031
HCV-1	1a	GTTGTGACCTCGACCCCCAAGCCCCGGTGGCCATCAAGTCCCCTCACCGAG	
HCV-J	1b	-T-G-C---G----A-G---G---A-	
BE90	1b	-T-G-C---G-G---A-ACA---A---G-A-	
2TY4	1c	-GC---G-C-A---T---AAAT---T---	
4TY4	1c	-GC---G-C-A---CT---AAAT---T---	
HC-J6	2a	-TC-T-GCC-GAGG-G---A-ACT---AC-C-A-G---T---	
HC-J8	2b	-TCT---GCCT-AAG---A-AACT-T---AC-C-G---T---	
NE91	2b	-TC---GCC---AAG-G---A-AACT-T---AC-C-G---T---	
EB12	2b	-TC---GCC-T-AAG-G---A-AACT' T---AC-C-G---T---	
ARG6	2c	-TCA---GCC-TGAGG-G---T-AACT---AC-C-A-G---T---	
ARG8	2c	-TCA---GCC-GAGG-G---T-AACT---T---AC-C-A-G---T---	
I10	2c	-CTCA---GCC-TGAGG-G---A-ACT---T---AC-C-A-G---T---	
T983	2c	-TCA---GCC-T-AGG-G---T---GACT---T---AC-C-AT-G---T---	
NE92	2d	-CTCTT-ACC-GAG-G---A-GACT---AC-C-A-G---T---	
CHR20	3a	-C---A---T---A-GG-G---A-GAAA-TG---TCC---G---G-	
CHR21	3a	-C---A---T---A-GG-G---A-GAAA-TG---TCC---G---G-	
CHR22	3a	-C---A---T---A-GG-G---A-GAAA-TG---TCC---G---G-	
T1	3a	-C---A---T---A-GG-G---A-GAAA-TG---TCC---G---G-	
T7	3a	-C---CA---T---A-GG-G---A-GAAA-TG---TCC---G---G-	
NE93	3a	-C---A---T---A-GG-G---A-GAAA-TG---TCC---G---G-	
NZL13	3a	-C---A---T---A-GG-G---A-GAAA-TG---TCC---G---G-	
EB1	3a	-C---A---T---A-GG-G---A-GAAA-TG---TCC---G---G-	
EB2	3a	-C---A---T---A-GG-G---A-GAAA-TG---TCC---G---G-A	
EB3	3a	-C---A---T---A-GG-G---A-AAAAA-TG---TCC---G---G-	
EB7	3a	-C---A---T---A-GG-G---A-GAA-TG---TCC---G---G-	
BR33	3a	9,11	G---G-
BR34	3a	1,3	A---G---A
BR36	3a	5,7	G---G-
T9	3b	-C---T---G---AG-G---T---CAA---G---GCG-T---A---	

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Figure 1 - Continued 3

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Figure 1 - Continued

		AGGCTTTATGTTGGGCCCTTACCAATTCAAAGGGGGAGAACTGGGG
HCV-1	1a	C-----C-----A-----C-----T-----C-----G-----T-----A-----C-----C-----T-----
HCV-J	1b	C-----C-----A-----C-----T-----C-----G-----T-----A-----T-----A-----C-----C-----T-----
BE90	1b	-AT-G-C-C-A-G-C-G-CT-G-T-----A-----T-----A-----C-----C-----T-----
2TY4	1c	-AT-G-C-C-T-G-C-T-----A-----T-----A-----C-----C-----T-----
4TY4	1c	-A-----C-----G-----A-----G-----CA-GTT-----CAGC-A-----CC-----C-----
HC-J6	2a	-A-----C-----A-----A-----G-----CA-G-A-----CAGC-AA-----CATC-----
HC-J8	2b	-A-----C-----G-----A-----G-----CA-G-TA-----CAGC-AA-----CATC-----
NE91	2b	-A-----C-----C-----A-----G-----CA-G-A-----CAGC-AA-----CATC-----
EB12	2b	-A-----C-----C-----A-----G-----CA-G-A-----CAGC-AA-----CATC-----
ARG6	2c	-G-----C-----A-----G-----CA-G-A-----CAGC-AA-----CATC-----
ARG8	2c	-A-----A-----C-----A-----G-----CA-G-A-----CAGC-AA-----CATC-----
I10	2c	-A-----G-----C-----A-----G-----CA-G-A-----CAGC-A-----CATC-----
T983	2c	-A-----A-----C-----G-----A-----G-----CA-GCTA-----CAGC-AA-----CA-C-----
NE92	2d	-C-----G-----A-----G-----CA-GCTA-----CAGC-AA-----CA-C-----
CHR20	3a	C-----CTGC-----A-----G-----GT-----CAGC-A-----CCC-G-----T-----
(CHR21	3a	C-----CTGC-----A-----G-----GT-----CAGC-A-----CCC-G-----T-----
CHR22	3a	C-----CTGC-----A-----G-----GT-----CAGC-A-----CCC-A-----T-----
T1	3a	C-----CTGC-----A-----G-----GT-----CAGC-A-----CCC-G-----T-----
T7	3a	C-----CTGC-----A-----G-----GT-----CAGC-A-----CCC-G-----T-----
NE93	3a	C-----CTGC-----A-----G-----GT-----CAGC-A-----CCC-G-----T-----
NZL13	3a	C-----CTGC-----A-----G-----GT-----CAGC-A-----CCC-G-----T-----
EB1	3a	C-----CTGC-----A-----G-----GT-----CAGC-AA-----CCC-G-----T-----
EB2	3a	C-----CTGC-----A-----G-----GT-----CAGC-AA-----CCC-G-----T-----
EB3	3a	C-----CTGC-----A-----G-----GT-----CAGC-A-----CCC-G-----T-----
EB7	3a	C-----CTGC-----A-----G-----GT-----CAGC-AA-----CCC-G-----T-----
BR33	3a	C-----CTGC-----A-----G-----GT-----CAGC-A-----CCC-G-----T-----
BR34	3a	C-----CTGC-----A-----G-----GT-----CAGC-AA-----CCC-G-----T-----
BR36	3a	C-----CTGC-----A-----G-----GT-----CAGC-AA-----CCC-G-----T-----
T9	3b	C-----CA-C-----A-----T-----CA-GTA-----CTCC-G-----

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Figure 1 - Continued 5

T10 BE98	3b 3c	C-----G--CA-C--A--T--CA-GTA---CAGT-A---CTCC-G----- C-----CTG---T--A-GTT---CAGC-A---AC-AC-----
GB48	4c	--A--C--C--G--C--T--CA-GCAT--CAGC-A---A--CCTG-----
GB116	4c	--A--C--C--G--C--T--CA-GCAT--CAGC-A---A--CCTG-----
GB215	4c	--A--C---G---C---T--CA-GCAT--AGC-AA---A--CCTG-----
GB358	4c	--A--C---G---C---T--CA-GCAT--CAGC-A---A--CCTG-T--
GB809	4e	--A--C--C--G--C--CA-GCAT--CAGC-A---A--CCTG-T--T--
CAM600	4e	--A--C--C--G--C--A-GTA---AGC-A---A--CCTT-----
CAMG22	4f	--A--C---G---C---T--CA-GCA---CAGC-A---A--CCTA-----
GB549	4g	--A--C--C--G--C--T--CA-GTA---C-C-A---CCTA-----
GB438	4h	--A--C--CAAG---C---CA-GTAT--CAGC-A---A--CCTA-----
CAR4/1205	4i	--A--C--C--G--C--A-GCA---CAGC-A---A--CCTG-T--
CAR1/501	4j	--A--C---G---C---A--CA-GTT---CAGC-A---A--CCTG-----
EG-13	4k	--A--C--C--G--C---CA-GCA---CAGC-A---A--CCTT-T--
EG-19	4k	--A--C--C--G--C---CA-GCA---AGC-A---A--CCTT-T--
BR95	5a	C-C--C---CTG---A---CA-GTA---CAGC-A---C-AC-G---T--
BE96	5a	C-CT-G-TCTG---A---CA-GTAT---CAGC-A---C-AC-A---T--
CHR18	5a	C-C--G---CTG---A---CA-GTAT---CAGC-A---C-AC-A---T--
CHR19	5a	C-C--G---CTG---A---CA-GTAT---CAGC-A---C-AC-A---T--

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Figure 1 - Continued 6

		8082	8131
HCV-1	1a	CTATCGCAGGTGCCGGCGAGCGGGTACTGACAACTAGCTGTGGTAACA	
HCV-J	1b	T-----C-----A-----T-----G-----G-----C-----C-----C-----	
BE90	1b	-----C-A-----A-----G-----G-----C-----C-----T-----	
2TY4	1c	-----T-----C-----C-----C-----C-----C-----C-----C-----	
4TY4	1c	-----T-----C-----G-----G-----T-----C-----C-----C-----	ATG--G--
HC-J6	2a	G--CA-GC-T-----C-----G-----T-----C-----C-----C-----	
HC-J8	2b	-----CA-GC-T-----A-----T-----TT-C-----C-----C-----	ATG--G--T-
NE91	2b	T--CA-GC-T-----A-----T-----TT-C-----C-----C-----	
EB12	2b	T--CA-GC-C-----A-----T-----TT-C-----T-----C-----	AATG--G--T-
ARG6	2c	G--CA-GC-T-----A-----G-----C-----C-----C-----	ATG--G--T-
ARG8	2c	G--CA-GC-T-----CA-G-----C-----C-----C-----C-----	ATG--C--
I10	2c	G--CA-GC-T-----A-----G-----C-----C-----C-----	ATG--C--
T983	2c	T--CA-GC-T-----TG-G-----C-----C-----C-----	ATG--C--
NE92	2d	A--CA-AC-C-----C-----A-GT-C-----C-----	ATG--A--T-
CHR20	3a	T----C-T-----T-----T-----A-----C-----C-----TC--C--	
CHR21	3a	T----C-T-----T-----T-----A-----T-----C-----TC--C--	
CHR22	3a	T----C-T-----T-----T-----A-----T-----C-----TC--C--	
T1	3a	T----C-----T-----C-----T-----A-----C-----C-----TC--C--	
T7	3a	T----C-----T-----C-----T-----A-----T-----C-----TC--C--	
NE93	3a	T----C-----T-----T-----C-----T-----A-----T-----C-----TC--C--	
NZL13	3a	T----C-----T-----T-----C-----T-----A-----T-----C-----TC--C--	
EB1	3a	T----C-----T-----T-----C-----T-----A-----T-----C-----TC--C--	
EB2	3a	T----C-----T-----T-----C-----T-----A-----T-----C-----TC--C--	
EB3	3a	T----C-----T-----T-----C-----T-----A-----T-----C-----TC--C--	
EB7	3a	T----C-----T-----T-----C-----T-----A-----T-----C-----TC--C--	
BR33	3a	T----C-----C-----T-----C-----T-----A-----T-----C-----TC--C--	
BR34	3a	T----C-----T-----T-----C-----T-----A-----T-----C-----TC--C--	
BR36	3a	T----C-----T-----C-----T-----C-----T-----C-----TC--C--	
T9	3b	T----C-----C-----C-----C-----C-----C-----C-----TC--C--	

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Figure 1 - Continued 7

T10	3b	8082	C-C-----C-----CT--C-T-C-----TC--C--T-
BE98	3c	T-C---C-C-----T-T-G--G--AC-C-----TC-G--	-
GB48	4c	G-----A--T-----A-----CTAC--C-----TC--G--	-
GB116	4c	G-----A-----T-----CTAC--C-----TC--G--	-
GB215	4c	G-----A-----A-----CTAC--C-----TC--G--	-
GB359	4c	G-----A-----A-----CTAC--C-----TC--G--	-
GB809	4e	G-----T-----A-----TAC--C-----TC--G--	-
CAM600	4e	G-----A-----A-----TAT--C-----TC--G--	-
CAMG22	4f	G-----C-----T-----A-----TAC--C-----TC--G--	-
GB549	4g	GC-A-----G-----A-----G-----CTAC--C-----TC--G--	-
GB438	4h	GCT-----G-----A-----G-----TAC--C-----TC--G--	-
CAR4/1205	4i	-ATC-----T-----A-----T'TAC--C-----TC--A--	-
CAR1/501	4j	AC-A-----C-----A-----GT-C-----C-----TC--G--	-
EG-13	4k	G-----G-----A-----A-----CT-T-----G-----TC--A--	-
EG-19	5a	G-----C-----A-----G-----A-----CTAT--G-----TC--A--	-
BE95	5a	T-----A-----C-----T-----C-----CT-C-----TATG-C--	-
BE96	5a	T-----A-----C-----C-----C-----CT-C-----TATG-C--	-
CHR18	5a	T-----T-----A-----C-----C-----CT-C-----TATG-C--	-
CHR19	5a	T-----C-----T-----A-----C-----C-----TATG-C--	-

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Figure 1 - Continued 8

	8132	8181
HCV-1	CCCTCACTTGCTACATCAGGGCGGGCAGGCCCTGTCGAGCCGCAGGGCTC	
HCV-J	-A-T-T-G--ACT--G-----T---AA-----	
HC-J6	-A-G-A-T-----TT-----G-----A-----	
HC-J8	-A-G-G-T-----A-----TT-----G-----AA-----	
NE91	-A-G-A-----A-----TT-----G-----CAA-----T-----A-----	
EB12	-A-G-----A-----G-G-A-TAAA-----G-----AAC-----G-----CA-T	
ARG6	-A-G-----C-C-A-----A-----G-----AAC-----G-----CA-T	
ARG8	-G-----G-----G-G-A-----A-A-G-----G-----AAC-----G-----CA-T	
I10	-A-T-G-T-----G-G-A-----AA-----G-----AAC-----G-----CA-T	
T983	-A-G-----G-G-----AA-----G-----CAAC-----TG-----CA-T	
NE92	-AA-----T-----TA-A-G-----T-GAAG-----C-----	
CHR20	-AA-----T-----TA-A-G-----TGCGAAG-----C-----	
CHR21	-AA-----T-----TA-A-G-----TGCGGAAG-----C-----	
CHR22	-AA-----T-----A-TA-A-G-----TGCGGA-----C-----	
T1	-AA-----T-----ACA-G-----TGC-GAAG-----C-----	
T7	-GA-----T-----ACA-G-----TGCAA-G-----C-----	
NE93	-AA-----T-----ACAA-G-----GCGAAAG-----C-----	
NZL13	-AA-----T-----ACA-G-----TGC-AAG-----AAC-----	
EB1	-AA-----T-----A-TACA-G-----CGAG-----C-----	
EB2	-AA-----T-----ACA-G-----CGAG-----C-----	
EB3	-AA-----T-----ACA-G-----CAA-----C-----	
EB7	-MA-----T-----ACA-G-----TGCAAA-----C-----	
BR33	-AA-----T-----ACA-G-----TGCAAA-----C-----	
BR34	-MA-----T-----ACA-G-----GCAA-----C-----	
BR36	-AA-----T-----ACA-G-----GCAA-----C-----	
T9	-AA-A-C-T-----ACT-----A-CA-G-----T-G-T-----	

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Figure 1 - Continued 9

		8132	8181
T10	3b	-AA-A--C--T-----ACT--G---A-CA-G--T--G--T---	
BE98	3c	-AA---C--T-----A--AAA---TACCAA---T--C--AA-T	
GB48	4c	-A--G--G-----C----A---TCA--C--TATCAA---G--G--G	
GB116	4c	-A--G--G-----TC---A---TCA--C--TATCA---G--G--G	
GB215	4c	-A--G--G-----TC---A---TCA--C--ATCA-G--GT-----G	
GB353	4c	-A--G--G-----C---A---TCA--C--TATCA---G--G--G	
GB809	4e	-AA-G--G-----C-T----TCA---ATCA-G--T--G--A	
CAM600	4e	-A--G--G-----C-T--A---TCA---ATCA-G--T--G--G	
G22	4f	-T--G--G-----T-C----ACA--G--ACCAA---T--C--A	
GB549	4g	-TG-A--G--T--TC---GTT--G--TAC-A-G-----T--G	
GB438	4h	-GG-G--A-----C-T--A---ACA---ACCA-G--T--G	
CAR4/1205	4i	-G--G-----C--A---ACA--G--ACCA-G-----CT-G	
CAR1/501	4j	-A--G--G-----C-T--A---ACA--T--TAC-A--A--C--CT-A	
EG-13	4k	-G--G--G-----C-A--AC--C--TAT-A--G--G--G	
EG-19	4k	-G--G--G-----C--A---ACA--C--TAT-A--G--G--A--A	
BE95	5a	--A-G--G-----TTA--CT-----A-----A-----A-----A	
BE96	5a	--A-G--G-----T--TPA--CT-----A-----A-----T-----	
CHR18	5a	--A-G--G-----T--TPA--CT-----A-----AA-----A-----	
CHR19	5a	--A-G--G-----TTCA--C-----A-----T-----AA-----	

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Figure 1 - Continued 10

HCV-1	8182	CAGGACTGGACCATGGCTCGTGTGGCGACGACTTAGTCGTTATCTGTGA	8231
HCV-J	1a	ATT-CGCC-A-G-A-C-T-C-A-C-	-
HC-J6	1b	ATT-CGCC-G-A-A-C-T-C-A-C-	-
HC-J8	2a	ATT-CGCC-G-T-G-A-C-T-C-A-C-	-
NE90	2b	ATT-CGCC-G-T-G-A-C-T-C-A-C-	-
2TY4	1b	ATT-CGCC-G-T-G-A-C-T-C-A-C-	-
4TY4	1c	ATT-CGCC-A-G-A-C-T-C-A-C-	-
HC-J8	2b	ATT-CGCC-G-T-G-A-C-T-C-A-C-	-
NE91	2b	ATT-CGCC-G-T-G-A-C-T-C-A-C-	-
EB12	2b	ATT-CGCC-G-T-G-A-C-T-C-A-C-	-
ARG6	2c	ATT-CGCC-G-T-G-A-C-T-C-A-C-	-
ARG8	2c	ATT-CGCC-G-T-G-A-C-T-C-A-C-	-
I10	2c	ATT-CGCC-G-T-G-A-C-T-C-A-C-	-
T983	2d	ATT-CGCC-G-T-G-A-C-T-C-A-C-	-
NE92	3a	-G-A-CCGGA-T-T-C-C-A-T-C-G-G-G-C-	-
CHR20	3a	-G-AC-CCGGA-T-T-C-C-A-T-C-G-G-G-C-	-
CHR21	3a	-G-A-CCGGA-T-T-C-C-A-T-C-G-G-G-C-	-
CHR22	3a	-G-A-CCGGA-T-T-C-C-A-T-C-G-G-G-C-	-
T1	3a	-G-A-CCGGA-T-T-C-C-A-T-C-G-G-G-C-	-
T7	3a	-G-A-CCGGA-T-T-C-C-A-T-C-G-G-G-C-	-
NE93	3a	-G-A-CCGGA-T-T-C-C-A-T-C-G-G-G-C-	-
NZL13	3a	-G-A-CCGGA-T-T-C-C-A-T-C-G-G-G-C-	-
EB1	3a	-G-A-CCGGA-T-T-C-C-A-T-C-G-G-G-C-	-
EB2	3a	-G-A-CCGGA-T-T-C-C-A-T-C-G-G-G-C-	-
EB3	3a	-G-A-CCGGA-T-T-C-C-A-T-C-G-G-G-C-	-
EB7	3a	-G-A-CCGGA-T-T-C-C-A-T-C-G-G-G-C-	-
BR33	3a	-G-A-CCGGA-T-T-C-C-A-T-C-G-G-G-C-	-
BR34	3a	-G-AG-CCGGA-T-T-C-C-A-T-C-G-G-G-C-	-
BR36	3a	-A-A-CCCAT-TT-C-T-C-A-T-C-G-G-A-C-	-
T9	3b	-A-A-CCCAT-TT-C-T-C-A-T-C-G-G-A-C-	-

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Figure 1 - Continued 11

		8182	8231
T10	3b	A-A---CCAT--T-C--T--C--C--A---T--G--G---G-C---	
BE98	3c	A-AA-TCCCAT-AT-C--T--C--C--A--T--G--G---G-TGC---	
GB48	4c	AGA-----T-G--C---T--T--C-G--T--C---GC---	
GB116	4c	AGA-----T-G--C---T--T--C-G--C---TGC---	
GB215	4c	AGA-----T-G--C-A---T--C-G---C---TGCC-	
GB358	4c	AGA-----T-G--C---T--C-G---C---GC-	
GB809	4e	A---T-----G--T--C--T--C---G---GCC-	
CAM600	4e	A-----G--T--C--T--C---G---GCC-	
G22	4f	A-----T G-----T-----G-----GC---	
GB549	4g	A-A-GT-----G--T--A-----C-----C-C-	
GB438	4h	A-A-T-----G--A--C--T-----TGCC-	
CAR4/1205	4i	A---T-----G--C--C--N-----C-G--T--C--TGC-	
CAR1/501	4j	A-A-T-----G--C--C--T-----T--CC--	
EG-13	4k	AGA-----T-----T-----TC-T--G-CC---C-	
EG-19	4k	A-A--A-----T-----G-----GC-C--G-----T-----TCAT--G-CC---C-	
BE95	5a	-G-----A-----GC-C--G-----T-----T-----TC-T--G-CC---C-	
BE96	5a	-----GC-C--G-----T-----T-----T-----G-CC---T-C-	
CHR18	5a	-----GC-C--G-----T-----T-----G-CC---T-C-	
CHR19	5a	-----GC-C--G-----T-----TTAC--G--G-CC---T-C-	

SUBSTITUTE SHEET (RULE 26)

Figure 1 - Continued 12

HCV-1	8232
HCV-J	AAGCGCGGGGTCCAGGAGGACGGGGAGCCTGAGAGCC
BE90	G-T---AAC---T---GC---AC---AC---AC---
HC-J6	G---CA---AC-G---A-CG---A-----
HC-J8	G---CAA---TAA-G---A-CGA-A-----
NE91	G---CA---TAA-G---A-CGA-A-----T
NE92	G---TCA---AC-G---A-CG---A-----
CHR20	G---T-AT---C---G-C---TAGA---AGC-----
CHR21	G---T-AT---C---G-C---TAGAA---AGC---C-----
CHR22	G---T-AT---C---A-T---TAGA---AGC---G-----
T1	G---AT---C---G-T---TAGA---AGC-----
T7	G---T-AT---C---G-C---TAG-A---GC-----
NE93	G---T-AT---C---G-C---TAGA---AGC-----
NZL13	G---T-AT---C---G-T---TAGA---AGC-----
BR33	G---T
BR34	G---T
BR36	3a-----TGC---C---G---AGA---AGCT---C-----
T9	3b-----TGC---C---G---AGA---AGCT---C-----
T10	3b-----T---A---G-T---AGA---
BE98	3c-----

SUBSTITUTE SHEET (RULE 26)

Figure 1 - Continued 13

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Figure 2

<u>Figure 2</u>	SEQ ID	2645	2694
HCV-1	1a	STVTESDIRTEEAIYQCCCDLDPQARVAIKSLTERLYVGGPLTNSRGGENCG	
HCV-J	1b	--N-----S-----A-E--Q--R-----K-Q--	
BE90	1b	--N---V--S-----A-E--Q-----K-Q--	
2TY4	1c	-----H-D-----N-----K-----	
4TY4	1c	-----H-D-A-N-----K-----	
HC-J6	2a	-----R-----S--RA-S-PEE-HT-H-----MF--K-QT--	
HC-J8	2b	-----R-----S--A-S-PQE-TV-H-----M--K-QS--	
NE91	2b	-----R-----S--A-S-PQE-TV-H-----M--K-QS--	
EB12	2b	-----A-S-PQE-TV-H-----M--K-QS--	
ARG8	2c	-----S-S-PEE-T-H-----M--K-QS--	
I10	2c	-----LS-S-PEE-T-H-----M--K-QS--	
T983	2c	-----A-S-PQE-T-H-----M--K-QS--	
NE92	2d	-----R-----S--LA-S-PE-T-H-----ML--K-QT--	
CHR20	3a	-----Q--V--E----N-E-E--KV-S-----C----MF--K-AQ--	
CHR21	3a	-----Q--V--E----N-E-E--KV-S-----C----MF--K-AQ--	
CHR22	3a	-----Q--V--E----N-E-E--RV-S-----C----MF--K-AQ--	
T1	3a	-----Q--V--E----N-E-E--KV-S-----C----MF--K-AQ--	
T7	3a	-----Q--V--E----N-E-E--KV-S-----C----MY--K-VQ--	
NE93	3a	-----Q--V--E----N-E-E--KV-S-----C----MF--K-AQ--	
NZL13	3a	-----Q--V--E----N-E-E--KV-S-----C----MF--K-AQ--	
EB1	3a	-----N-E-E--KV-S-----C----MF--K-AQ--	
EB2	3a	-----N-E-E--KV-S-----C----MF--K-AQ--	
EB3	3a	-----N-E-E--KV-S-----C----MF--K-AQ--	
EB7	3a	-----N-E-E--KV-S-----C----MF--K-AQ--	
BR33	3a	10,12	-----C----MF--K-AQ--
BR34	3a	2,4	-----C----MF--K-AQ--
BR36	3a	6,8	-----C----MF--K-AQ--
T9	3b	-----H-----E-----E-E--K--SA-----I--MY--K-LQ--	
T10	3b	-----Q-----E-----E-E--K--SA-----I--MY--K-LQ--	
BE98	3c	150	A-----KDE--RV-T-----C----MF--K-QH--

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Figure 2 - Continued 1

		2645	2694
EG13	4a	V----N-E-E--K-TA--	MH--K-DL--
EG19	4a	V----S-ELE--KV-TA--	MH--K-DL--
GB48	4C	-----K---V--EV-----	MH--K-DL--
GB116	4C	-----K---V--EV-----	MH--K-DL--
GB215	4C	-----K---V--EV-----	MH--K-DL--
GB358	4C	-----K---V--EV-----	MH--K-DL--
GB809	4e	-----R--KV--EV-----	MH--K-DL--
CAM600	4e	-----R--V--EV-----	MH--K-DL--
CAMG22	4f	-----R--V--EV-----	MH--K-DL--
GB549	4g	-----R--E--KV-AA--	MH--K-DL--
GB438	4h	-----R--V--E--KV-TA--	MY--K-DL--
CAR4/1205	4i	P----R-X-V--EV----	MH--K-DL--
CAR1/501	4j	P----R-X-R--GEV----	MF--K-DL--
BE95	5a	-----H--M--S--Q--E--A--R--Q--C--MY--K-QQ--	
BE96	5a	-----A--H--L--S--SQ--D--A--R--Q--FC--MY--K-QQ--	
CHR18	5a	-----H--M--S--SLY--Q--E--R--Q--C--MY--K-QQ--	
CHR19	5a	-----H--M--S--SLY--Q--E--A--R--Q--C--MY--K-QQ--	

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Figure 2 - Continued 2

	2695	YRRCRASGVLTSCGNTLTCYIKARAACRAAGLQDCTMLVCGDDLVVTCI
1a	-	-
1b	-	-
1b	-	-
1c	-	-
1c	-	-
2a	M--I--V--L--K--IIAP-	S-
2b	F--M--M--L--K--IV-PV-	S-
2b	F--M--M--L--K--IV-PV-	S-
2b	F--M--M--L--K--IV-PV	S-
2c	A--M--V--N--IVAP-	-
2c	M--V--N--IVAP-	-
2c	V--M--V--K--N--IVAS-	-
2d	F--M--I--V--Q--K--IIAP-	S-
3a	P--F--I--SK--RNPDF--	VA-
3a	P--F--I--AK--RTPDF--	VA-
3a	P--F--I--AE--RNPDF--	VA-
3a	P--F--I--T--AK--RNPDF--	VA-
3a	P--F--I--T--A--RNPDF--	VA-
3a	P--F--I--T'T--AK--RNPDF--	VA-
3a	P--F--I--T--AK--N--RNPDF--	VA-
3a	P--F--I--T--E--RNPDF	-
3a	P--F--I--T--E--RNPDF	-
3a	P--F--I--T--K--RNPDF	-
3a	P--F--I--T--K--RNPDF	-
3a	P--F--I--T--AK--RNPDF--	VA-
3a	P--F--I--T--A--RNPDF--	VA-
3a	P--F--I--T--AK--RSPDF--	VA-
3b	P--F--I--T--K--PSF--	VS-
3b	P--F--I--T--K--PSF--	VS-
3c	P--F--I--K--TKNPSF--	VA-

Figure 2 - Continued 3

	2695	2744
GB48	4C	-Y---F---L---S---IK---R---
GB116	4C	-Y---F---L---S---I---R---
GB215	4C	-Y---F---L---S---I---S---R---
GB358	4C	-Y---F---L---S---I---S---R---
GB809	4e	-Y---F---M---L---S---I---K---
CAM600	4e	-Y---F---L---S---I---K---
CAMG22	4f	-Y---F---FL---T---TK---K---
GB549	4g	-Y---F---V---L---V---T---KG---S---
GB438	4h	L---Y---F---V---L---T---T---K---
CAR4/1205	4i	I---Y---F---V---L---T---T---K---
CAR1/501	4j	Q---F---E---L---T---T---K---
EG13	4k	F---F---L---T---I---R---
EG19	4k	Y---F---L---T---I---K---S---
BE95	5a	F---M---M---L---S---R---R---L---
BE96	5a	F---M---M---L---S---T---R---Y---L---
CHR18	5a	F---M---M---L---S---K---L---
CHR19	5a	F---M---M---S---K---L---VT---A---

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Figure 2 - Continued 4

		2745	2757
HCV-1	1a	SAGVQEDAASLRA	
HCV-J	1b	- - - T - - - A - - -	
BE90	1b	- - - T - - - - V	
HC-J6	2a	- Q - TE - - ERN - - -	
HC-J8	2b	- Q - NE - - ERN - - -	
NE91	2b	- Q - NE - - ERN - - -	
NE92	2d	- Q - TE - - ERN - - -	
CHR20	3a	- D - - D - - R - A - - -	
CHR21	3a	- D - - D - - RTA - - -	
CHR22	3a	- D - - N - - R - A - G -	
T1	3a	- D - - D - - R - A - - -	
T7	3a	- D - - D - - RTA - - -	
NE93	3a	- D - - D - - R - A - - -	
NZL13	3a	- D - - D - - R - A - - -	
BR33	3a	-	
BR34	3a	-	
BR36	3a	-	
T9	3b	- C - - E - - R - A - - -	
T10	3b	- C - - E - - R - A - - -	
BE98	3c	- - - ID - - R - -	

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Figure 2 - Continued 5

GB48	4C	2745	2757
GB116	4C	-D--E--KRP-G-	-D--E--KRA-G-
GB215	4C	-D--E--KRA-G-	-D--E--KRA-GV
GB358	4C	-D--E--KRA-G-	-D--E--KRA-G-
GB809	4e	-G--E--KRA-G-	-G--E--KRA-G-
CAM600	4e	-G--E--KRA-G-	-G--E--KRA-G-
G22	4f	-D--E--RRA-G-	-D--E--RRA-G-
GB549	4g	-G--E--RA--	-G--E--RA--
GB438	4h	-G--E--RA--	-I-ID--KQA-T
CAR4/1205	4i	-I-ID--KQA-T	--E--PXTX-P
CAR1/501	4j	--E--PXTX-P	
BE95	5a	-Q-TH--E----	
BE96	5a	-Q-TH--E-N---	
CHR18	5a	-Q-TH--K----	
CHR19	5a	-Q-TH--E-C--V	

SUBSTITUTE SHEET (RULE 26)

Figure 3

	SEQ ID	1
HCV-1	1a	ATGAGGCCACGGAAACTCCTAAACCTCAAAAAAAACAAACGTAAACACCAACCG
HCV-J	1b	-A-----
HC-J6	2a	-A-----
HC-J8	2b	-A-----
NE92	2d	143
EB1	3a	-A-----
NZL1	3a	-ACT--
HCV-TR	3b	-ACT--
BE98	3c	-ACT--
GB358	4c	147
GB809	4e	191
CAM600	4e	163
GB724	4?	165
EG-29	4?	193
BE95	5a	151
		51
		TCGCCCACAGGACCGTCAAGTTCCGGGTGGGGTCAGATCGTTGGTGGAG
HCV-1	1a	-C-----
HCV-J	1b	-T-----
HC-J6	2a	-A-----
HC-J8	2b	-T-----
NE92	2d	-C-----
EB1	3a	-C-----
NZL1	3a	-A-----
HCV-TR	3b	-A-----
BE98	3c	-G-----
GB358	4c	-CAT-----
GB809	4e	-CAT-----
CAM600	4e	-TAT-----
GB724	4?	-TAT-----
EG-29	4?	-CAT-----
BE95	5a	-T-----

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Figure 3 - Continued 1

		101
HCV-1	1a	TTTACTTGGTGCAGGGGCCAGGGCCCTAGATTGGCTGTGGCGACGAGA
HCV-J	1b	-----C-----C-G-----T-G-----
HC-J6	2a	-A-----C-----G-----A-G-----
HC-J8	2b	-----C-----C-----A-G-----
NE92	2d	-----A-----CC-G-----G-----
EB1	3a	-A-----G-----T-----C-T-----
NZL1	3a	-A-----G-----AC-----C-T-----
HCV-TR	3b	-A-----TG---C-----T-----AGTAC-T-----
BE98	3c	-----G-C-A--A-----T-----AGT-C-C-----
GB358	4c	-----CCAG-----C-G-----T-G-----
GB809	4e	-----G-----G-----TC-G-----
CAM600	4e	-----C-----G-----TC-G-----
GB724	4?	-----CC-G-----TC-G-----
EG-29	4?	-----GA-----TC-G-----
BE95	5a	-----GA-----TC-G-----
		151
HCV-1	1a	AAGACTTCGAGGGTCAACCTCGAGGTAGACGCTATCCCCAA
HCV-J	1b	-----T-----A-----G-----A-----
HC-J6	2a	-----G-----C-----G-----C-----T-----
HC-J8	2b	-----T-----A-----C-----G-----C-----G-----
NE92	2d	-----A-----C-----G-----A-----T-----G-----C-----
EB1	3a	-----A-----T-----A-----G-----C-----AC-----A-----
NZL1	3a	-----A-----T-----A-----G-----C-----AC-----A-----
HCV-TR	3b	-----G-----G-----CAAACAG-----C-T-----
BE98	3c	-----CA-----G-----C-----A-----C-----G-----
GB358	4c	-----G-----T-----G-----G-----C-----A-----
GB809	4e	-----G-----T-----G-----G-----C-----A-----
CAM600	4e	-----G-----T-----C-----G-----A-----
GB724	4?	-----G-----T-----G-----C-----A-----A-----
EG-29	4?	-----G-----T-----G-----C-----A-----A-----
BE95	5a	-----G-----A-----C-----G-----T-----

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Figure 3 - Continued 2

201

HCV-1	1a	GGCTCGTCGGCCGAGGGACCTGGCTCAGCCGGTACCCCTGGC
HCV-J	1b	C-----T-----C-----A-----G-----CT-----ACT-----A-----GAA-----A-----A-----A-----C-----
HC-J6	2a	-A-----G-----CT-----ACT-----AAT-----GAA-----A-----A-----A-----T-----
HC-J8	2b	A-----A-----G-----CT-----ACC-----A-----T-----GAA-----A-----A-----A-----
NE92	2d	A-----A-----G-----C-----ACT-----A-----T-----GAA-----A-----A-----A-----
EB1	3a	G-----G-----AG-----A-----T-----G-----G-----AG-----A-----T-----
NZL1	3a	G-----G-----AG-----A-----C-----T-----G-----C-----G-----
HCV-TR	3b	CTC-----G-----C-----T-----G-----C-----AA-----T-----G-----C-----AA-----T-----
BE98	3c	G-----A-----AT-----T-----A-----T-----A-----A-----T-----
GB358	4c	G-----C-----AT-----AT-----G-----C-----AT-----G-----
GB809	4e	G-----C-----AA-----AT-----G-----C-----AA-----G-----
CAM600	4e	G-----C-----T-----T-----G-----AG-----A-----T-----
GB724	4?	G-----C-----AT-----A-----T-----A-----A-----A-----T-----
EG-29	4?	G-----C-----A-----AC-----C-----T-----G-----A-----
BE95	5a	
	251	CCCTCTATGGCAATGAGGGCTGGGGATGGCTCCCTGTCTCCC
HCV-1	1a	C-----C-----TATG-----A-----A-----A-----A-----
HCV-J	1b	A-----C-----G-----ACT-----C-----A-----A-----
HC-J6	2a	G-----C-----A-----T-----C-----A-----T-----C-----
HC-J8	2b	G-----C-----G-----CT-----C-----A-----G-----C-----
NE92	2d	T-----C-----T-----A-----G-----A-----G-----C-----A
EB1	3a	T-----C-----A-----T-----A-----G-----A-----C-----
NZL1	3a	C-----G-----A-----T-----A-----G-----A-----C-----
HCV-TR	3b	A-----G-----A-----A-----G-----A-----G-----C-----G
BE98	3c	T-----T-----C-----T-----T-----A-----G-----A-----G
GB358	4c	T-----T-----C-----T-----T-----A-----G-----C-----T
GB809	4e	T-----C-----T-----T-----A-----G-----C-----T
CAM600	4e	T-----C-----T-----T-----A-----G-----C-----T
GB724	4?	
EG-29	4?	T-----T-----C-----T-----T-----A-----G-----C-----T
BE95	5a	

Figure 3 - Continued 3

301		CGTGGCTCTGGCCTAGGGCCCCACAGACCCCCGGGTAGGTCGCG									
1a	HCV-1	-	-	-	-	-	-	-	-	-	-
1b	HCV-J	-	-	-	-	-	-	-	-	-	-
2a	HC-J6	-A--	T--	C--	T--	CTCT	-	-	-	A--	C-
2b	HC-J8	-C--	G--	T--	CT	-	-	-	A--	A--	-
2d	NE92	-A--	G--	C--	GTCA	-	-	-	AC--	A--	-
3a	EB1	-C--	C--	C--	T--	ATCT	-	-	A--	C--	-
3a	NZL1	-C--	C--	T--	ATC	-	-	-	A--	A--	-
3b	HCV-TR	-T--	C--	C--	T	-	-	-	G--	C--	-
3c	BE98	-C--	C--	C--	GTCG	-	-	-	A--	C--	-
4e	GBB809	-C--	G--	-	GTCT	-	-	-	G--	C--	-
4e	CAM600	-C--	N--	-	N-GTCT	-	-	-	AT--	A--	-
4?	GB724	-C--	-	-	ATCT	-	-	-	A--	G--	-
5a	BE95	-A--	-	-	AT	-	-	-	A- -AA-	A- -AA-	-
351		CAATTGGGTAAGGtCATCGATAACCCTAACGTGGGTTGCCGACCTCA									
1a	HCV-1	-	-	-	-	-	-	-	-	-	-
1b	HCV-J	-	-	-	-	-	-	-	A-	-	-
2a	HC-J6	-	-	-	-	-	-	-	T--	-	-
2b	HC-J8	-	-	-	-	-	-	-	A--	-	-
2d	NE92	-	-	-	-	-	-	-	T--	-	-
3a	EB1	-	-	-	-	-	-	-	T--	-	-
3a	NZL1	-	-	-	-	-	-	-	C--	-	-
3b	HCV-TR	-	-	-	-	-	-	-	A--	-	-
4e	GBB809	-	-	-	-	-	-	-	A--	-	-
4e	CAM600	-	-	-	-	-	-	-	A--	-	-
4?	GB724	-	-	-	-	-	-	-	G--	-	-
5a	BE95	-	-	-	-	-	-	-	T--	-	-

Figure 3 - Continued 4

HCV-1	1a	401	TGGGGTACATACCGCTCGTCGGCCCCCTCTGGAGGCCGTGCCAGGGCC
HCV-J	1b		- - - - T - - - - C - A - G -
HC-J6	2a		- - - - C - TG - - A - - G -
HC-J8	2b		- - - - C - TG - - T - - - - A - T
NE92	2d		- - - - C - TG - - AG - - T - - T - - A - T
NZL1	3a		- - - - C - - - T - - G - A - - A -
HCV-TR	3b		- - - - T - - - G - G - - TC - - A - A -
GB809	4e		- - - - A - - C - - T - A - - CG - G - T - - A -
CAM600	4e		- - - - A - - C - - T - A - - CG - G - T - - T C -
GB724	4?		- - - - A - - C - - G - - CG - C - G - - T C -
BE95	5a		- - - - T - - C - - - A - - G - - CA - - - TC - - A - - T
SUBSTITUTE SHEET (RULE 26)			
HCV-1	1a	451	CTGGCGCATGGCGTCCGGTTCTGGAAAGACGGCGTGAACATATGCAACAG
HCV-J	1b		- - - - A - - - T - - - G -
HC-J6	2a		- - C - - - GA - A - - C - - - G - - - G - T - T -
HC-J8	2b		- - A - - C - - T - - TA - - G - - - GA - A - T - C -
NE92	2d		- - C - - - GA - A - - GA - A - - GA - A -
NZL1	3a		- - C - - - GA - - CC - - T - - - GA - A - - T - TC -
HCV-TR	3b		- - C - - - T - - - T - - GA - - CA - - T - GG - - A -
GB809	4e		- - - A - - C - - T - - TA - - C - G - - GA - C - - C -
CAM600	4e		- - - A - - T - - TA - - C - G - - GA - C - T - -
GB724	4?		- - - A - - C - - G - - GA - T - - N - G - -
BE95	5a		- - C - - A - - C - - T - - GA - - - C - - T - - G - - - C - - A -

Figure 4

	SEQ ID NO	379 ACGTGGGCTTCGCCAACCTCATGGGTACATACCGCTCGTGGGCC	428
HCV-1	1a		
HCVEC1	1a		
HCVHCT18	1a		
HCVHCT23	1a		
HCVHCT27	1a		
HCVTH	1a		
HCV-J	1b		
HC-J6	2a	C--TG---A-	
HC-J8	2b	C--TG---T-	
NE92	2d	C--TG	
HD10	3a	T-----T	
BR33	3a	T-----T	
BR36	3a	T-----T	
NZL15	3a	C-----C	
HCV-TR	3b	T-----T	
GB809_4	4a	A-----C-----G	
GB116	4c	189	
GB215	4c	183	
GB358	4c	185	
GB809_2	4e	118, 187	
CAM600	4e	122, 169	
CAMG22	4f	167	
CAMG27	4f	171	
GB549	4g	173	
GB438	4h	120, 175	
CAR1/1205	4i	177	
		179	
		SUBSTITUTE SHEET (RULE 26)	

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Figure 4 - Continued 1

CAR4/901	4?	181	G-----T-----A-----C-----A-----
BE95	5a	143	-----A-----T-----C-----A-----G-----
BE100	5a	195	-----A-----A-----C-----G-----

Figure 4 : Continued 2

		429	478
HCV-1	1a	TC TTGGAGGCGCTGCCAGGGCCCTGGCGCATGGGGTTCTGGAAAG	
HCVEC1	1a		
HCVHCT18	1a		
HCVHCT23	1a		
HCVHCT27	1a		
HCVTH	1a		
HCV-J	1b		
HC-J6	2a	G-C-C-TC-A-T-C-GA-A-C-G-	
HC-J8	2b	GG-TC-A-T-C-TA-C-G-	
NE92	2d	AG-T-T-TC-A-T-C-GA-A-	
HD10	3a	-G-A-TC-A-A-T-GA-CC-T-	
BR33	3a	CG-A-TC-A-A-T-GA-CC-T-	
BR36	3a	CG-A-TC-A-A-T-GA-CC-T-	
NZL15	3a	-G-A-TC-A-A-C-GA-CC-T-	
HCV-TR	3b	-G-G-G-TC-A-A-C-T-T-GA-CA-T-GG-	
GB809 ₄	4a	CG-G-TC-A-A-T-GA-C-G-G-	
GB116 ₋	4c	-G-G-T-TC-A-AA-C-T-TA-C-G-G-	
GB215	4c	CG-G-T-TC-A-AA-C-T-TA-C-G-G-	
GB358	4c	-G-G-T-TC-A-C-T-TA-C-G-G-	
GB809 ₂	4e	CG-G-T-TC-A-C-T-TA-C-G-G-	
CAM600	4e	CG-G-T-TC-A-C-T-TA-C-G-G-	
CAMG22	4f	-G-G-T-TC-A-T-C-A-C-G-G-	
CAMG27	4f	-G-G-T-TC-A-T-C-A-C-G-G-	
GB549	4g	-G-G-T-TC-A-T-C-A-CCG-G-	
GB438	4h	AG-A-TC-A-T-A-C-G-G-	
CAR4/1205	4i	CG-G-TC-AR-T-A-C-G-	

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Figure 4 : Continued 3

CAR4 / 901	4?	CG-G--T---TC---A-----C--T--TA---C-G--G-
BE95	5a	CG---G---TC---A----T---C---A---C---T---GA---C---T---G-
BE100	5a	CG---G---TC---A----T---C---A----T---GA---T---GA---T---G-

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Figure 4 : Continued 4

		479	528
HCV-1	1a	ACGGCGGTGAACACTATGCCAACGGGAAACCTTCCTGGTTCTTCTATC	
HCVEC1	1a		
HCVHCT18	1a		
HCVHCT23	1a		
HCVHCT27	1a		
HCVTH	1a		
HCV-J	1b		
HC-J6	2a	--G-T-T-T-A-C-C-T-	
HC-J8	2b	--GA-A-T-C-TT-A-C-C-T-	
NE92	2d	--GA-A-G-C-T-G-C-C-T-	
HD10	3a	--GA-A-T-TC-TT-G-C-C-T-	
BR33	3a	--GA-A-TC-TT-G-C-C-T-	
BR36	3a	--GA-A-T-TC-TT-G-C-C-T-	
NZL15	3a	--GA-A-T-TC-TT-G-C-C-T-	
HCV-TR	3b	--A-T-T-T-G-C-C-T-	
GB809_4	4a	--GA-T-G-T-C-C-T-	
GB116_	4c	--TA-T-T-T-C-C-T-	
GB215	4c	--A-C-T-T-C-C-T-	
GB358	4c	--GA-C-T-G-T-C-C-T-	
GB809_2	4e	--GA-C-C-T-T-C-C-T-	
CAM600	4e	--GA-C-T-C-T-C-T-	
CAMG22	4f	--GA-T-C-C-T-	
CAMG27	4f	--GA-A-C-C-T-	
GB549	4g	--GA-T-C-C-T-	
GB438	4h	--GA-C-C-T-C-T-	

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Figure 4 - Continued 5

CAR4/1205	4 i	----GA-C--T-----T-
CAR4/901	4?	----GA-T-----C-----T-
BE95	5a	----G-A-----C-----TT-A-C-----T-G-----T-
BE100	5a	----G-----T-----T-----G-----T-----T-G-----T-

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Figure 4 : Continued 6

		578
HCV-1	1a	529
HCVEC1	1a	TTCCTTCGGCCCTGCTCTTGACTGTGCCCGCTTCGGCTACCA
HCVHCT18	1a	- - - - - T - - - - -
HCVHCT23	1a	- - - - - C - - - - -
HCVHCT27	1a	- - - - - A - - - - -
HCVTH	1a	- - - - - A - - - - -
HCV-J	1b	- - - - - A - - - - -
		- - - - - C - - - - -
HC-J6	2a	- - - - - G - - - - -
HC-J8	2b	- - - - - T - - - T - - -
S83	2c	- - - - - G - - - - -
NE92	2d	- - - - - G - - - - -
		- - - - - C - - - - -
HD10	3a	- - - - - T - - - T - - -
BR33	3a	- - - - - T - - - T - - -
BR36	3a	- - - - - T - - - T - - -
NZL15	3a	- - - - - A - - - T - - -
HCV-TR	3b	- - - - - G - - - T - - -

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Figure 4 - Continued 7

GB809_4	4a	529	- - - C - - - A - - T - - G - - - C - C - - - C - - A - - G - - A - - TG - G - -
Z4	4a		G - G - -
Z1	4b		GTG - -
GB116	4c		- C - - CT - - A - - T - - G - - - C - - - T - - A - C - - A - - GT - A -
GB215	4c		- A - - CT - - A - - T - - G - - - C - - - T - - A - C - - AT - -
GB358	4c		- - - CT - - A - - T - - G - - - C - - - T - - A - C - - GT - A -
Z6	4c		GT - A - - GTTA -
Z7	4c		- - - A - -
DK13	4d		- - - CT - - A - - T - - G - - - C - - - T - - G - - - G - GTTA -
GB809_2	4e		- - - CT - - G - - C - - - T - - A - A - - GTTA -
CAM600	4e		- - - A - - T - - G - - - C - - - C - - - TGTG - -
G22	4f		- - - A - - T - - G - - - C - - - C - - - C - - A - - TGTG - -
G27	4f		- - - A - - T - - G - - - C - - - C - - - GC - G - -
GB549	4g		- - - CT - - TA - - T - - GC - - C - A - - C - - G - T - - TC - G - -
GB438	4h		- - - C - - T - AA - - T - - G - - C - - - T - - C - - A - - AT - -
CAR4/1205	4i		- - N - - - A - - T - - G - - C - - - C - - G - - C - - TC - G - -
CAR4/901	4?		- - TA - - - T - - T - - - G - - TC - - - C - - T - - AGTT - C
BE95	5a		- - A - - - T - - A - - T - - G - - C - - C - - T - - AGTT - C
BE100	5a		GT - C
SA4	5a		

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Figure 4 - Continued 8

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Figure 4 - Continued

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Figure 4 - Continued 10

		629	CGAGTATTGTGTACGAGGGCGGATGCCATCCTGCACACTCGGGGTGC	678
HCV-1	1a	-	-	T
HCVEC1	1a	-	-	T
HCVHCT18	1a	-	-	T
HCVHCT23	1a	-	-	T
HCVHCT27	1a	-	-	T
HCVTH	1a	-	-	T
HCV-J	1b	-	-	T
HC-J6	2a	AT--C--	ACC-GGC-ACTCCAG-C--TG--	C----
HC-J8	2b	AC--C-	CACC-GGC-CTCA-T-C--AG-T-C-TCT--	T-A--
S83	2c	-T--C--	T-GGC-C'T'-AA-CA--AC-C--T--T--A--	T-A--
NE92	2d	GT--C--C--	GGC-CTCAGG--TG-T--T-G-T--GTC-C-----	T
SUBSTITUTE				
HD10	3a	GC-----	T-----C-AT--C-TT--T-----A--C--C--T	
(BR33	3a	GT-----	T-----C-AT--C-TT--T-----G-G--C--C--T	
(BR36	3a	GC-----	C-AT--C-TT--T-----A--C--C--T	
NZL15	3a	GC-----	T-----C-AT--T-----A--C--C--T	
HCV-TR	3b	G-----	C-AA---TG---TTA--C--A--	

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Figure 4 - Continued 11

		678
GB809_4	4a	-C--CG-A--C--T--AA-T-A-C-CCAT--AT--TTG--
Z4	4a	-C--A--C--T-A-C--CA--A--TTG--
Z1	4b	-C--C--A--A--AGC-CCA--A--TTG--A--T
GB116	4c	-C--A--A--T-A-T-CCA--A--CTC--T
GB215	4c	-C--A--A--C-A-CCA--A--CT--A
GB358	4c	-C--A--A--A-C-AGC-CCA--A--CTC--A
Z6	4c	-C--A--T--C-AAC-CCAG--T-A--CTC--A
Z7	4c	-C--AA--T--C-AAC-CCA--A--CTC--A
DK13	4d	-C--A--C--T--AA-C-ATT-CCA--T-A--CTC--A
GB809_2	4e	-C--A--A--A-C-A-A--CA--T-A--CTC--A
CAM600	4e	-A--C--A--A-C-AA--CA--T-A--CTC--A
G22	4f	-T--C--A--C-TT--A-T-C--CA--T--CT--A--A
G27	4f	-T--C--A--C-TT--A-AGC--CA--T--TCT--A--A
GB549	4g	-T--A--T-A-C--CAT--A--TCTA--A--T
GB438	4h	-C--T--A--C-A-C-CA--A--CTA--C--T
(CAR4/1205	4i	-T--C--A--T--A--C-AGA-CCA--T--CT--T
CAR4/901	4?	-C--C--A--T--A--C-ATC-CCA--A--TTA--A
BE95	5a	-TTCC--A--C--T----A-ATA-CCTG----A--G-A--T--T--
BE100	5a	-TTCC--A--C--T----A-AT--CTG----A--G-A--T--C--
SA4	5a	-TTCC--A--T----T-ATA-CCTG----T-G-A--T--T--

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Figure 4 - Continued 12

HCV-1	1a	679	GTCCCTTGCCTCGTAGGGCAACGCCCTCGAGGTGGTGGCATGAC	728
HCVEC1	1a		- - - - - AC - - - - T	
HCVHCT18	1a		- - - - - AC - - - - T	- - - G - - -
HCVHCT23	1a		- - - - - C - - - - AT - - - A	- - - G - - -
HCVHCT27	1a		- - - - - C - - - - T	- - - AA - - -
HCVTH	1a		- - - - - C - - - - T	- - - C - - - AG - - -
HCV-J	1b		- - - G - - - C - - - A - - T - - TTT - - CC - T - - A - - C - C - -	
HC-J6	2a		- - - G - - - AGAAA - T - - - G - - TA - A - - TC - - - C - - - A - AC - - G - CT - -	
HC-J8	2b		- - - A - - T - AGAA - - - TAATGG - A - - - T - CAT - - C - - A - ACAAG - A - -	
S83	2c		- - - T - AG - - - ACC - C - - - T - - - TC - A - - - C - - G - TG - -	
NE92	2d		- - - T - AGGAGA - - - ATA - - CC - C - - - A - AC - - G - TT - -	
HD10	3a		- - A - - - T - - - AG - - - C - - - TA - A - - TGC - - - C - - - ACCC - AG - - -	
BR33	3a		- - A - - - T - - - C - AG - - - C - - - TA - G - - T - CA - - C - - - ACCC - AG - A - -	
BR36	3a		A - A - - - T - - - C - AG - - - C - - - TA - A - - C - C - - - C - - - ACCC - AG - - -	
NZL15	3a		- - A - - - T - - - C - AG - - - C - - - TA - A - - T - C - - - C - - - ACCC - AG - - -	
HCV-TR	3b		- - G - - C - - - CACAACC - - - CAA - - ATCA - - C - - - ACAA - - G - CT - -	

Figure 4 - Continued 13

		679	728
GB809_4	4a	--A--C---GA-G-CC--G---TG---TC-T-C---AC-C-G-A-	
Z4	4a	--A--C---T---GATGACT--G---A-A---C-T---C---AC-C-G---	
Z1	4b	--C---T---G---GAC---AG---TA-T---TC-C---C---C-CT---	
GB116	4c	T-A--C---GA-G-TT--G---TCAG---AC-C---C---CC-T-	
GB215	4c	T-A--C---T---GA-G-TT--G---TCAG---AC-T---CC-CT-	
GB358	4c	T-A--C---GA-G-TT--G---TCAG---AC-C---C---CC-C--	
Z6	4c	T-G--C---T---GA-G-TT--G---TCAG---AC-C---C---CC-T-	
Z7	4c	--A--C---T---GA-G-G---G---CAG---AC-C---C---CC-T-	
DK13	4d	--T---GA-G-A---G---AAC---T---CA-C---T---TC-C--	
GB809_2	4e	--A--C---T---GAAGACC---G---CAG---C---CC-C--	
CAM600	4e	--A--C---T---GA-GACT---G---CAG---C---CC-C--	
G22	4f	--T---AA-AACT---G---CAG---TC---C---A---CT---	
G27	4f	--C---T---GA-AACT---G---CAG---AC-A---C---A-A---CT-	
GB549	4g	-G---GA-AACC---G---A---C-C---C---TC-TT-A--	
GB438	4h	--G---C---T---AA-AACT---G---T-T---C-T---A-TC-TT-A--	
CAR4/1205	4i	A-A---C---T---GAAGACC---G---TCAG---C---C---TC-C--	
CAR4/901	4?	A-A---C---GA-GACC---G---TT---C-C---C---AT-TC---	
BE95	5a	--G---T---CATGACA---T---T-TGAGT---A---C---CCAA-T--	
BE100	5a	--G---T---CA-GA-A-AT---T-TGAGT---C---CCAA-T--	
SA4	5a	--G---T---CA-GC-A-AT---T-TAGT-A---C---CCAA-C--	

Figure 4 - Continued 14

		729	778
HCV-1	1a	CCCTACGGTGGCACCAAGGATGGCAAACCTCCCCGGACGGCAGCTTCGAC	
HCVEC1	1a	--C-----C-----A-----A-----	
HCVHCT18	1a	--C-----C-----A-----A-----	
HCVHCT23	1a	--C-----C-----A-----A-----	
HCVHCT27	1a	--C-----A-----C-----A-----	
HCVTH	1a	--C-----C-----C-----A-----	
HCV-J	1b	T--C---C-C-GG-A-CA-GCA-A-C-ACAA-A-----	
HC-J6	2a	A--G-AT-----GTGCA-C-GCC-GCCGCC-T-A-CA-GGCT-A--GA	
HC-J8	2b	A--C-AC---TGTG-AAC-CC--GGTAGCG-T-A-TCGTAGC-G--A	
S83	2c	--C-ATC-C---TA--ACCTGGCGCT-T-A-T-A-GGC-G--G	
NE92	2d	G--C-ATA-A-TGTG-CC-ACCTGGTGCG-TTA-C-A-GGC-G--GA	
HD10	3a	A-----A-----AGT-----T-C-GG-GCAA-A-CG-TTC-A-A--CA	
BR33	3a	A-----A-----AGT-----T-C-T-GGGCAA-A-CG-TTC-A-A--CA	
BR36	3a	A-----A-----AGT-----A-T-C-T-GG-GCAA-A-CG-TTC-A-A--CA	
NZL15	3a	A-----A-----AGT-----T-C-T-GG-GCAA-TA-TG-TTC-A-A--CA	
HCV-TR	3b	AA-G-----GTT---ACCCCTTGGCG-GA-A-CG-TC-A-C--A	

Figure 4 - Continued 15

		729	778
GB809_4	4a	A-----TG--GTATCCCATGG-CGCT--GCTCGA-TCCCT-C--G-	
Z4	4a	G-----A----TGT-GCAC-CCGGGGCGCT--GCTTGA-TC-T-C--G-	
Z1	4b	-C---T----G-GCCCT--CC--CGCA-G--CA	
GB116	4c	T-C--C----GG-GCCCTT-C-TTGGGTGCT--GCTAGAATCC--C--GA	
GB215	4c	T-C--C----GG-GCCCTT-CAT-GGTGCT-A-TTGAATCCCT-C--GA	
GB358	4c	T-C--C----GG-GCCCTT-CAT-GGCCT-GCTTGAATCC--C--GA	
Z6	4c	T-C--C----GGTGTCTT--AT-GGTGCT-GCTTGAATCCC--C--GA	
Z7	4c	T-C--C----GG-GCCCTT--AT-GGTGCA-GCTTGAATCCA-C--GA	
DK13	4d	-C---C----TG-GCAAAC--CTG--TGCT--GCTTGA-TCTT-GA--	
GB809_2	4e	T-C--A----GT-GCCTT-C-T-GGTGCT-GCTCGA--CCT-G--G-	
CAM600	4e	T-C--A--GT-GCCAT-C-C-GGTGCT-GCTTGA--CCT-G--G-	
G22	4f	-C---C----G-GCCAT-CCT'GGCGCT--ACTCGA-TCCA-G--G-	
G27	4f	-C---T----G-GCCAC-CATTGGCGCT--ACTTGA-TCCA-G--G--	
GB549	4g	A---C---T---TG--CCCT--TGTGGCGG-GCTTGAATCCA-G--G-	
GB438	4h	A---C---T--A---GT-CCCT-CCT-GGGGCT--ACTT--TCTG-A--G-	
CAR4/1205	4i	-C---C---GG--CCAC'-CCT'ACGTGCT--GCTTT-TCCA-A--GG	
CAR4/901.	4?	A---T----TG-TCCCT-CCT-GGGGCT--GCTT--TC---A--G-	
BE95	5a	-C---AC--T--AG--CC-AGCCT-GG-GCAGT-A--G-T-CTT--GA	
BE100	5a	-C---C--T--AG--CC-AGCCTT-GG-GCAGT-A--G-T-CC--GA	
SA4	5a	-C---T--AG--CC-GCAGT-A--G-T-CTT--GA	

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Figure 4 - Continued 16

	779	828
HCV-1	GTCACATCGATCTGCTTGTGGAGGCCACCCCTCTGGCCCTCTAC	-C-----
HCVEC1	-	-C-----
HCVHCT18	1a	-C-----
HCVHCT23	1a	-C-----
HCVHCT27	1a	-T-----
HCVTH	1a	-T-----
HCV-J	1b	-C-----
HC-J6	2a	CG-----T--CA--G----GAT--TC--G-----C--C--T--T--
HC-J8	2b	CA-----G--CA--A-C--AAT-GCA--T--GGC-----C-----T-G-T
S83	2c	CA-----A-CA-C--GAT-TCT--T--GG-----T-----T-----T
NE92	2d	CG---T---T---ACCA-CA-T-CATC---T---GTP-T---C---T---G-----
HD10	3a	-G---TG-A--CA--T-G--G---CGCG-----GA-G--C--T--T--
BR3	3a	--TG-G--C---T-A--A--CGCG-----GA-G--C--T--G-----
BR3	3a	--TG-G--C--AT-A--G---CGCG-----GA-G--C--T--G-----
BR3	3a	--TG-G--C--AT-A--A--CGCG-----GA-G--C--T--G-----
NZL15	3a	CC---TG-G--A---G--A--CGCACGACAA--G-----G--G-----
HCV-TR	3b	

Figure 4 - Continued 17

		779	828
GB809_4	4a	-G--TG-G--C--AA-G--A--TGGCG--	-G-G--T-T-
Z4	4a	-A--TG-G--CT-AA-G--A--CGCG--	TT-G--T-
Z1	4b	-G--TG-A--C--A-G--G--TGGCG--	C--T--
GB116	4c	--TG-G--A-G--A-G--A--TGCT--	C-C-T-T-
GB215	4c	-A--G-G--CA--A-G--C--CGCT--	C-C-T-T-T-
GB358	4c	--TG-G--A-G--A-G--TGC--	T--TGGG--C-C-T-T-
Z6	4c	-A--TG-G--C--A-G--G--CGCT--	T--TG-A-C-T-
Z7	4c	-A--TG-G--C--A-G--A--CGCT--	T--AG-G-C-C-T-
DK13	4d	--TG-G--C--A-G--G--CGCT--	T--AT-G-C-C-C-
GB809_2	4e	-C--TG-G--C--A-G--A--TGCT--	G-G-C-C-C-
CAM600	4e	--TG-G--C--A-G--A--TGCT--	A-G-C-C-C-
G22	4f	--TG-G--T--A-G--G--C-CT--	T--AT-G-C-A-A-
G27	4f	--TG-G--T--A-G--A--C-CT--	AT-G-C-C-A-
GB549	4g	-G--G-G--CT-AA-G--G--TGC--	G-C-G-C-
GB438	4h	AG--TG-G--C--A-G--G--GGG--	T-A-C-T-T-
CAR4/1205	4i	CG--TG-G--C--AA-G--G--GGCA--	C-C-TT-T-
CAR4/901	4?	-G--TG-G--T--A-G--G--TGCA--	T-C-T-
BE95	5a	-AGC-G-T--CTAC-A-CG--AG-G--	TG-C-C-GT-A--
BE100	5a	-AGC-G-T--TACT-G--G--AG-G--	TG-C-C-GT-A--
SA4	5a	-GGC-G-T--CTACT-A-CG--AG-G--	TG-C-C-A-A--

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Figure 4 - Continued 18

		878
HCV-1	1a	GTGGGGACCTATCGGGTCTGTCGCCAACTGTTCACCTT
HCVEC1	1a	- - - - G - - - - C - - - - T - - - - T - - - -
HCVHCT18	1a	- - - - T - G - - - - T - - - - T - - - -
HCVHCT23	1a	- - - - T - G - - - - CA - - - - T - - - -
HCVHCT27	1a	- - - - T - G - - - - T - - - - T - - - -
HCVTH	1a	- - - - G - - - - CA - - - - T - - - -
HCV-J	1b	- - T - - T - C - - A - - C - - T - - C - - - -
HC-J6	2a	- - - - C - - - - TGGG - - GA - G - - - - CA - C - - - -
HC-J8	2b	- - - - A - - TG - G - - - - G - C - - GA - - C - ATCG - - GGCT - - - - TGG - -
S83	2c	- - - - G - G - - T - - CG - GC - GA - G - - G - C - - CT - - GG - CG - - GT - G - -
NE92	2d	A - A - - A - - G - - T - - CG - G - - GA - GT - G - CTTCT - - G - C - - - T - A - -
HD10	3a	- - - - T - TA - G - - T - - G - C - - C - - C - - G - - - -
BR33	3a	- - - - T - TA - G - - T - - G - C - - C - - A - - GCC - - - -
BR36	3a	- - - - T - - A - G - - T - - G - - - - C - - C - - G - - - -
NZL15	3a	- - - - T - TA - G - - T - - G - - - - C - - G - - A - - GCC - - - -
HCV-TR	3b	- - C - - - GCT - T - - G - - - - G - - - - G - - A - - GC - - - -

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Figure 4 - Continued 19

		829	878
GB809_4	4a	--T--A-----C---T---AGG---CT---C---A---G---GA-----	
Z4	4a	--T-----C-----AGG---C---GA---G---GA---A-----T---	
Z1	4b	A-T--A---T---G---T---AGGC-----C---A---G-----GA-----	
GB116	4c	A-C-----G-----TGGC---A---T---G---T---GA-----TT-T-	
GB215	4c	A-T-----T---G---T---TGGC---A---CT---G---T---GA-----TT-T-	
GB358	4c	A-C-----G-----TGGC---A---T---G---T---GA-----T-T-	
Z6	4c	--T--A---T---G---TGG---CA---CT---G---T---GA-----T-----	
Z7	4c	A-T-----G-----TGGC---A---T---G---T---GA-----TP-T-	
DK13	4d	A-C---A---G---T---GG---G---CT---G-----T-----	
GB809_2	4e	--C---C---G-----TGGCT-A---CT---G---A-----A-----	
CAM600	4e	A-C---C---T---G-----TGGCT-A---CT---G---G-----A-----	
G22	4f	--T-----G-----GGCA---A---C---A---CG-----GA-----	
G27	4f	A-T---A---T---G-----AGGCA---A---A---G-----GA-----	
GB549	4g	A-C---A---T-----AGG-----C---G-----GA-----	
GB438	4h	A-C---A---AT-----AGG-----CT---G---CA---G-----GT-----	
CAR4/1205	4i	A-T---A---T---G-----GG-----T---G---CG-----TA-----	
CAR4/901	4?	--C---A---C---T---AGG-----C---A---G-----GA-----	
BE95	5a	--A---A---GCG---T---G---AC-A---CT---G---A-----A-----A	
BE100	5a	--T---A---GCG---T---G---AC-A---T---G---A-----A-----A	
SA4	5a	--C---GCG---G---A---G---T---G---A-----A-----A-----A	

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Figure 4 - Continued 20

HCV-1	1a	879	CTCTCCCAGGCCACTGGACGACGCCAAGGTTGCAATTGCTCTATC	928
HCVEC1	1a			
HCVHCT18	1a			
HCVHCT23	1a			
HCVHCT27	1a			
HCVTH	1a			
HCV-J	1b			
HC-J6	2a			
HC-J8	2b			
S83	2c			
NE92	2d			
HD10	3a			
BR33	3a			
BR36	3a			
NZL15	3a			
HCV-TR	3b			

- A -- T C - C -- G T - T G A -- G T A -- A -- A -- -

- G -- A C A -- A -- T T T G T -- A C -- C -- C --

A -- A -- A C A A -- A A C T ' T C -- C -- T -- C --

G -- C -- A C A A -- A -- T A C - T T T G T C -- C -- T -- C -- A -- C --

G -- G -- C A -- A T -- T A A - T T T G T C -- G -- A C -- C -- T -- C -- A -- C --

A G A -- T C - T -- T C A A -- G T C -- G A C C -- T -- C -- A C -- G -- C --

A G A -- C -- C -- T C A A -- G T C -- G A C C -- T -- C -- G C -- G -- C --

A G A -- T C - T -- T C A A -- G T C -- G A C C -- T -- C -- G C -- G -- C --

A G A -- T C - A -- T C A A -- G T C -- G A C C -- T -- C -- G C -- G -- C --

A G A -- T C - C -- A C -- C G T -- G A C G -- C -- G -- A -- C --

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Figure 4 - Continued 21

GB809_4	4a	879	-CAG--GC-T-----C-----G-A---T-----C-----A
Z4	4a	TCGG--GC-T-----C-----G-AG-----T-C-----CA	
Z1	4b	-CGA--GC-C-G-----C-----C-G-A-----C-----C-----	
GB116	4c	-CAG--GC-A-----C-----G-AC-----T-----CG	
GB215	4c	-CGG--AC-A-----T-----G-AC-----T-----CG	
GB358	4c	-CAG--GC-G-----T-----G-AC-----T-----CG	
Z6	4c	-CAG--GC-A-----T-----G-AC-----T-----CG	
Z7	4c	-CAG--GC-A-----T-----G-AC-----T-----CG	
DK13	4d	-CAA--TC-C-----C-----C-C-----AC-----T-----CA	
GB809_2	4e	-CAA--GC-A-----C-----G-AC-----T-----CG	
CAM600	4e	-CAA--GC-A-T-----C-----T-G-AC-----T-----CA	
G22	4f	-GGG--C-C-T-----T-----C-----G-AG-----T-----C-----	
G27	4f	-AGG--C-C-TG-----C-----C-G-AG-----T-----C-----	
GB549	4g	-CGG--GC-C-----T-----T-----C-----C-----G	
GB438	4h	-CAA--C-C-T-----T-----C-----G-A-----T-----G	
CAR4/1205	4i	-CGG--AC-CATT--TGAA-----C-----T-----C-----CT	
CAR4/901	4?	-CAG--GC-C-----C-----T-----G-AC-----C-----T-----CG	
BE95	5a	TAGG--TC-C-AG---GCT---GT---GAAC-----C-----T-----CA	
BE100	5a	TAGG--TC-C-AG---TGCT---GT---G-AC-----C-----T-----CA	
SA4	5a	TAGG--TC-C-AG---ACT---GT---AC-----T-----CA	

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Figure 4 - Continued 22

		929
		CCGGCCATATAACGGGTCAACGGCATGGCA
HCV-1	1a	- - - - - C - - - - - G
HCVHCT18	1a	- - - - - - - - - - - - - - - - - -
HCVHCT23	1a	- - - - - - - - - - - - - - - - - -
HCVHCT27	1a	- - - - - - - - - - - - - - - - - A -
HCVTH	1a	- - - - - - - - - - - - - - - - - -
HCV-J	1b	- - - - - CG - - T - A - - - - - T
HC-J6	2a	- T - - T A C C - - C - - T - - A -
HC-J8	2b	A A - - T - - C - - C - - C - - T -
S83	2c	- G - - - G C - - T - - - A - - - T
NE92	2d	- A - - - C - - C - - T - - A - - T - G - - - G
HD10	3a	- A - - - - C - TT - A - - A - - - A - - - T
BR33	3a	- A - - - - C - TT - A - - A - - T - - A - - - T
BR36	3a	- A - - - - C - TT - A - - A - - T - - A - - - T
NZL1.5	3a	- A - - - - C - TT - A - - A - - T - - A - - - T
HCV-TR	3b	- A - - - - G - TT - A - - A - - T - - - T - - - G

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Figure 4 - Continued 23

		929	957
GB809_4	4a	-T-----C---C---A-G-----G	
Z4	4a	-T-----C---C---A-G-----G	
Z1	4b	-T---T---CG---CT-----C---A-G-----C	
GB116	4c	-G---G---CG---T-----C---A-G-----G	
GB215	4c	-G---G---C---C---T-----C---G-A-----G	
GB358	4c	-G---G---CG---T-----C---A-G-----G	
Z6	4c	-A---G---C-----C---A-G-----G	
Z7	4c	-G---G---CG---T-----A-C-----A-A-----G	
DK13	4d	-A---A---C---A---A---A-A-----T	
GB809_2	4e	-A---G---T-----C---T---G-----T	
CAM600	4e	-G-----C---T-----T---G-----G	
G22	4f	-G-----C---C-----TA---A-----G	
G27	4f	-A---C---C-----A-A-----G	
GB549	4g	AT-----C---C---C---TA---A-----T	
GB438	4h	TG-----C---C---C---A-G-----C	
CAR4/1205	4i	-A---G---C---C-----	
CAR4/901	4?	T-----C---C---A---A-----T	
BE95	5a	GT-----G-T---C---C-----G-----G	
BE100	5a	GT-----CG---C---C---T---AG-----G	
SA4	5a	GT-----C---C-----G-----G	

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Figure 5

	SEQ ID	1
HCV1	1a	MSTNPKPQKKNKRNTNRRPQDVKFPGGGQIVGGVYLLP R-T-----
HCVJ	1b	
HCJ6	2a	R-T-----
HCJ8	2b	R-T-----
NE92	2d	R-T-----
EB1	3a	R-T-----I-----V-----C-----
NZL1	3a	L-----R-T-----I-----V-----
HCV-TR	3b	L-----RQT-----L-----N-----V-----V-----
BE98	3c	L-----R-T-----X-----V-----Q-----V-----
GB358	4c	R-T-----M-----
GB809	4e	L-R-T-----M-----
CAM600	4e	R-T-----M-----
GB724	4?	R-T-----M-----
EG-29	4?	R-----M-----
BE95	5a	R-T-----M-----
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Figure 5 - Continued 1

		V-core
HCV1	1a	KTSERSQPRGRQQPIPKAR
HCVJ	1b	RPEGRTWAQ
HCJ6	2a	D--ST-KS-GK
HCJ8	2b	D--ST-KS-GK
NE92	2d	D--T-KS-GK
EB1	3a	S--S--
NZL1	3a	S--S--
HCV-TR	3b	KQ--IL--
BE98	3c	SR--S--
GB358	4c	T--S--
GB809	4e	S--S--
CAM600	4e	S--S--
GB724	4?	T--S--
EG-29	4?	S--S--
BE95	5a	Q-T--S-G--A---L---

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Figure 5 - Continued 2

	101	126
HCV1	RGSRPSWGP	
HCVJ	TDPRRRSRN	L
HCJ6	N-----H-----V-----	
HCJ8	T-----H-----R-----I	
NE92	H-----H-----	
NZL1	N-----N-----	
HCV-TR	N-----F-----	
BE98	N-----N-----	
GB809	N-----	
CAM600	-X-----X-----	
GB724	N-----N-----	
BE95	N-----N-----K-----	

Figure 5 - Continued 3

		127	TCGFADLMGYIPLVGGAPLGGAAARALAIIIGVRVLEDGVNYATGNLPGCSFSI	176
HCV-1	1a			
HCVEC1	1a			
HCVHCT18	1a		R	
HCVHCT23	1a			L
HCVHCT27	1a			
HCVT ^H	1a			
HCV-J	1b			
HC-J6	2a	V	V	F
HC-J8	2b	V	V	I
NE92	2d	V	V	I
HD10	3a	V	V	A
BR33	3a	V	V	I-F
BR36	3a	V	V	A
NZL1	3a	V	V	I-F
HCV-TR	3b	V	V	A-G

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Figure 5 - Continued 4

	127	176
GB809_4	4a	V-V-AV-I
GB116_-	4c	V-V-E-AV-I
GB215	4c	V-V-E-AV-I
GB358	4c	V-V-AV-I
GB809_2	4e	V-V-AV-I
CAM600	4e	V-V-AV-I
CAMG22	4f	V-V-AV-I
CAMG27	4f	S-V-AV-I
GB549	4g	V-V-AV-I
GB438	4h	V-V-AV-I
CAR4/1205	4i	V-V-AV-I
CAR4/901	4?	A-V-V-AV-I
BE95	5a	G-V-V-P
BE100	5a	G-V-V

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Figure 5 - Continued 5

		177	226
		E1 → V1	V2
HCV-1	1a	FLLALLSCLTVAPASA	YQVRNSTGLYIV
HCVEC1	1a	-----	S-----
HCVHCT18	1a	-----	H-----
HCVHCT23	1a	-----	-----
HCVHCT27	1a	-----	S-I---
HCVTH	1a	-----	-----
HCV-J	1b	I-----	E---VS-I---
HC-J6	2a	-----I-T-V--	AE-K-ISTG-M-
HC-J8	2b	-----V--V--	VE---ISSS-YA
S83	2c	-----I-V-G	VE-KDTGDS-MP
NE92	2d	-----L--K-TSSS-M-	-----Q-----
HD10	3a	F---III---AS	LEW--TS---VL
BR33	3a	F---III---AG	LEW--TS---VL
BR36	3a	F---III---AS	LEW--TS---VL
NZL1	3a	F---III---AS	LEW--TS---VL
HCV-TR	3b	F---C---G	LEYT-TS---VL
			S-----
			D-V----
			E-V---L
			PGC
			VYEAADAILHT
			TNDCPNSSI

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Figure 5 - Continued 6

		177	V1	V2	226
GB809_4	4a	---	EHY--AS-I--I	V---TDHH---L	---
Z4	4a	---	EHY--AS-I--I	DHH---L	---
Z1	4b	S---	VHY--AS-V--I	T---TEHH-M-L	---
GB116	4c	Y---	VNY--AS-V--I	DYH---L	---
GB215	4c	---	IHY--AS-V--I	DHH---L	---
GB358	4c	---	VNY--AS-I--I	TEHH---L	---
Z6	4c	---	VNY--AS-V--I	ELQ---L	---
Z7	4c	---	VNYH-AS-V--I	M---EHI---L	---
DK13	4d	G	-NY---S-V--I	TDYH---L	---
GB809_2	4e	---	VNY--AS-V--I	A---TDNH---L	---
CAM600	4e	---	VNY--AS-I--I	A---TENH---L	---
CAMG22	4f	---	VHYH-TS-I--L	F---VHH---L	---
CAMG27	4f	---	VHYH-TS-I--I	F---EHH---L	---
GB549	4g	---	QHY--IS-I--I	DHH-M-L	---
GB438	4h	V---R---	QHY--AS-I--I	DHH-M-L	---
CAR4/1205	4i	S---E---	IHY--ASDG-YI	ENH---L	---
CAR4/901	4?	X---	QHY--VS-I--I	DHH-M-L	---
BE95	5a	-I---	VPY--AS-I--I	DNL---A	---
BE100	5a	-I---	VPY--AS-I--I	D-L---A	---
SA4	5a	---	VPY--AS-V--I	DNL---A	---
HK2	6a	LTYG--S---L	-L---DAM---L	---	---

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Figure 5 - Continued 7

		227	V3	V4	276 PUTATIVE
HCV-1	1a	VPC	VREGNASRCWVAM	TPTVA	TRDGKLPATQ LRRHID LLVGSATLCSALY
HCVEC1	1a	-H-	-V-	-	-T-----
HCVHCT18	1a	-H-	-V-	-	-T-----
HCVHCT23	1a	-D-	-V-	-	-K-----
HCVHCT27	1a	-K-	-PV	A	-N-----
HCVTH	1a	-S-	-F-	-L-	-R-----
HCV-J	1b	-S-F-	-L-	-A-NSSI-T-T	-A-A---M-
HC-J6	2a	EKV--T	-IPV	S-N--	VQQPGALTQG --T--
HC-J8	2b	ENDNGTLH--	IQV	-N--	VKHRGALTTS --T-V-
S83	2c	E-TA-V	--PV	A-NL-	ISQPGALTKG --A--
NE92	2d	EEK--I	-IPV	S-NI-	VSQPGALTKG --T--
HD10	3a	-QD--T-A-	-TPV	-	V-YVGATTAS I---V-
BR33	3a	-QD--T-T-	-TPV	-	V-YVGATTAS I-S-V-
BR36	3a	I--	-QD--T-T-	-TPV	VKYVGATTAS I-S-V-
NZL1	3a	-QD--T-T-	-TPV	-	V-YVGATTAS I-S-V-
HCV-TR	3b	-TT-	Q-S--TTV	ST--	V-TLGVTTAS I-T-V-

Figure 5 - Continued 8

		227	V3	V4	PUTATIVE
GB809_4	4a	---	---	AVSMDA-LES	F---V-
Z4	4a	---	MT---T---TPV	VAHPGA-LES	F---V-
Z1	4b	---	TE---T---PL	APYPNA-LES	M---V-
GB116	4c	---	V---Q---L	APYVGA-LES	S---V-
GB215	4c	---	V---Q---L	APYIGA-VES	F---V-
GB358	4c	---	V---Q---L	APYIGA-LES	S---V-
Z6	4c	---	V---Q---L	VSYIGA-LDS	S---V-
Z7	4c	---	Q---L	APYIGA-LES	I---V-
DK13	4d	---	K-T---SL	AQILNA-LES	V-
GB809_2	4e	---	KT---Q---L	SPYVGA-LEP	V-
CAM600	4e	---	T---Q---L	SPYAGA-LEP	V-
CAMG22	4f	---	T---Q---L	APYLGA-LES	M---V-
CAMG27	4f	---	T---Q---I-L	APHIGA-LES	M---V-
GB549	4g	---	T---T---PL	APYVGA-LES	M---V-
GB438	4h	---	T---V---IPL	VPYLGA-L-S	V-Q-V-
CAR4/1205	4i	---	KT---Q---L	APHRLA-LSS	-A-V-
CAR4/901	4?	---	T---V---SL	APYLGAA-L-S	-V-
BE95	5a	---	MT---V---QI	APSLGAVTAP	---AV-
BE100	5a	---	KD---V---QI	APSFGAVTAP	---AV-
SM4	5a	---	QD---V---QI	APNLGAVTAP	---AV-
HK2	6a	---	VDDR-T---H-V	IPNAST---G	F---V-

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Figure 5 - Continued 9

		277	TRANSMEMBRANE DOMAIN	V5
HCV-1	1a	VGDLCGSVFLVGQLFTF	SPRRNIWTTQG	CNCSSIYPGHIITGHIRMA
HCVEC1	1a	-	-	-
HCVHCT18	1a	-	-	-
HCVHCT23	1a	-	I	D
HCVHCT27	1a	-	-	D
HCVTH	1a	-	I	-
HCV-J	1b	S	-	YE-V-D
HC-J6	2a	G-M-AA-M-IV	QII-FV-D	T
HC-J8	2b	V-A-MILS-A-MV	Q-NF-E	Q
SE3	2c	V-ALM-AA-VVVV	QII-TFV-E	R
NE92	2d	I-A-M-AS-V-II	QII-KFV-D	-
HD10	3a	M-A-A-A-A	Q-V-T	L-S
BR33	3a	M-A-A-A-A	Q-V-T	L-S
BR36	3a	M-A-A-A-A	Q-V-T	L-S
NZL1	3a	M-A-A-A-A	Q-V-T	L-S
HCV-TR	3b	AFA-A-A-A	T-V-T	VS

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Figure 5 - Continued 10

		277	TRANSMEMBRANE DOMAIN	V5	
GB809_4	4a		- - - - G A - - - M - -	Q - - - D - - - T - -	
Z4	4a		- - - - G A - - - M - - M I	R - - - E - - - T - -	
Z1	4b	I - - - G	D - R - - - D - -	V S - - -	
GB116	4c	I - - - G	S - Q - - - D - -	A - V - - -	
GB215	4c	I - - - G	S - R - - - D - -	A - A - G - -	
GB358	4c	I - - - G	S - Q - - - D - -	A - V - - -	
Z6	4c	I - - - G A - - - M - -	S - Q - - - D - -	A - A - - -	
Z7	4c	I - - - G	S - Q - - - D - -	A - V - - -	
DK13	4d	I - - - V - G - - -	Q - - - D - - - T - -		
GB809_2	4e	I - - - G L - - - M - -	Q - - - D - - - A - -		
CAM600	4e	I - - - G L - - - M - -	Q - - - D - - - T - -		
CAMG22	4f	I - - - G I - - - A - - M - -	R - - L - - - E - -		
CAMG27	4f	I - - - G I - - - M - - N -	R - - L - - - E - -		
GB549	4g	I - - - G - - - M - -	R - - D - - - D - -		
GB438	4h	I - - - H - - - A - - M V	S - Q - - - D - -	V - - -	
CAR4/1205	4i	I - - - G - - - A - -	- I R - - I - E - - D	S - - -	
CAR4/901	4?	I - - - G - - - M - -	Q - - - D - - - V - -		
BE95	5a	- - - A - - A L - - - M -	R - - Q - A - V - N	S - V - - -	
BE100	5a	- - - A - - A L - - - M -	R - - Q - A - V - D	S - V - Q - -	
SM4	5a	- - - A - - A - - - M -	R - - Q - T - V - D	S - - -	
HK2	6a	I - - - L - - A - - -	Q - - - V - D - - -	T - V - - -	

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Figure 6

4648 4698
 GTGCCAGGACCATCTTGAATTTGGAGGGCGCTTACAGGCCTCACT
 --C-----C-A-G-C-----A-----C-----C-----C
 -----A-----G-----CA-T-C-C-----A
 --A-T-A-C-G-G-C-----A-CG-----T-----A
 HCC153 -A-C-----A-----C-T-A-A-----
 EB1 4664
 EB2
 EB6
 EB7

4699 4750
 CATAAGATGCCCACTTCTATCCCAGACAAGCAGAGTGCCCCACCTT
 --C-----CT-G-----C-A-----GCA-A-C-----C
 --C-----C-T-----A-----ATCG-A-TT-C
 --C-T-C-----C-C-----G-----AG-A-A-A-T---
 --C-----G-A-----T-----CAG--ACTC-T-C
 HCC153 -----CAG--ACTC-T-C
 EB1 4731
 EB2
 EB6
 EB7

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Figure 6 - continued 1

<p>4751</p> <pre>CCTTACCTGGTAGCGTACCAAGCCACCGTAGGGCTCAAAGCCCC HCV-1 HCV-J HC-J6 HC-J8 HCCl53 EB1 EB2 EB6 EB7</pre>	<p>4800</p> <pre>A-----A-----A-----A-----G-----T----- C-----T-AAC---C-----G-----T-A-----CA----- G-G-T-AAAGG-C-----G-----A-A-----C-----AA-G----- T-G-T---ACT---C-----T-----A-----C-C-G-G-T----- T-G-----AACT---C-----T-----T-----CC-C-G-G-T-T T-G-----AACT---C-----T-----T-----CC-C-G-G-T-T T-G-----AACT---C-----T-----T-----CC-C-G-G-T-T T-G-----AACT---C-----T-----T-----CC-C-G-G-T-T</pre>	<p>4849</p> <pre>TCCCCCATCGTGGGACCAAGATGTGGAAAGTGTTTGTTCGCTCAAAGCCCC HCV-1 HCV-J HC-J6 HC-J8 HCCl53 EB1 EB2 EB6 EB7</pre>
---	---	--

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Figure 6 - continued 2

SEQ ID NO	4850	4900
HCV-1	CCCTCCATGGGCCAACACCCCCGCTATACAGACTGGGCCTGTTCAGAAT	
HCV-J	-A---G-----G-----G-----A---C---A---	
HC-J6	-A---GTG---C---C---T---C---G---C-CT-----T-----ACC---C	
HC-J8	-A---GAC---T---C---C---G---C---G---C-CT-----T---C---GACC---	
HCC153	29	-A---A---A---T---G---T---T---TC-GT-----GC-----C---A---
HD10-1-25	31	↑
HD10-1-3	33	-C---A---
BR36-20-164	35	-C---A---
BR36-20-166	37	-C---A---
BR36-20-165	39	-C---A---
EB1		-A---A---C---A---T---G---T-----TC
EB2		-A---A---A---T---G---T-----TC
EB6		-AT-A---A---C---G---T-----TC
EB7		-AT-A---A---C---G---T-----TC

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Figure 6 - continued 3

4949

4901 GAAATCACCCCTGACGCCAGTCACCAAATACATCATGCATGTC
 HCV-1 ---GG-----T---C---A-----CA-A-----G-----
 HCV-J ---GG-----C-----T---T---G---G-----GCC-C-----CA
 HC-J6 ---GG-----T-----C---G---G-----GCC-G-----CA
 HC-J8 ---GG-----T-----C---G---G-----GCC-G-----CA
 HCC153 -----TG-T-----A-----CA-----A-----G-----
 HD10-1-25 -----TG-T-----A-----C-----A-----T-----G-----
 HD10-1-3 -----TG-T-----A-----C-----A-----T-----G-----
 BR36-20-164 -----TG-T-----A-----CA-----A-----G-----
 BR36-20-166 -----TG-T-----A-----CA-----A-----G-----
 BR36-20-165 -----TG-T-----A-----CA-----A-----G-----

4990

4950 GGCGGACCTGGAGGTGGTCACGGCACCTGGGTGCTCGTTG
 HCV-1 -----T-----T-----A-----A-----A-----A-----
 HCV-J -----T-----A-----G-----C-----CT-A-C-----
 HC-J6 -----T-----A-----G-----A-----T-----C-----
 HC-J8 -----C-----A-----A-----G-----A-----T-----
 HCC153 A-----T-----T-----A-----AAC-----C-----T-GC-----
 HD10-1-25 A-----T-----T-----A-----AAC-----C-----T-GC-----
 HD10-1-3 A-----T-----T-----A-----AAC-----C-----T-GC-----
 BR36-20-164 A-----T-----T-----A-----AAC-----C-----TT-GC-----
 BR36-20-166 A-----T-----T-----A-----AAC-----C-----TT-GC-----
 BR36-20-165 A-----T-----T-----A-----AAC-----C-----TT-GC-----

Figure 6 - continued 4

4991 GCGGGCGTCTGGCTTGGCCGGTATTGCCTGTCAACAGGCTGCCGTG
 HCV-1A-----T---G---C-----C-----A-G-----A-----
 HCV-JA-----T---G---C-----C-----A-G-----A-----
 HC-J6G-----T---G---CG-C-----C-----G-G-----G-T-T-T
 HC-J8G-----G---A---C---CG-----A---T---C-----G-G-----A-T
 HD10-1-25 ...A-----G-----C---G---CC-A---G---C---C---T-----GTC-----T
 HD10-1-3A-----G-----C---G---CC-A---G---C---C---T-----GTC-----T
 BR36-20-164 ...A-----G-----C---G---CC-A---G---C---C---T-----GTC-----T-T-T
 BR36-20-166 ...A-----G-----C---G---CC-A---G---C---C---T-----GTC-----T-T-T
 BR36-20-165 ...A-----G-----C---G---CC-A---G---C---C---T-----GTC-----T-T-T

5041 GTCATAGTGGGAGGGTGGCTGTCCGGGAAGCGGGCAATCATACCTGA
 HCV-1
 HCV-J
 HCV-J6
 HCV-J8
 HD10-1-25
 HD10-1-3
 BR36-20-164
 BR36-20-166
 BR36-20-165

Figure 6 - continued 5

5091
 CAGGGAAAGTCCCTTACCGAGAGTTCGATGAGATGGAAAGAGTGCTCTCAGC
 HCV-1
 HCV-J
 HC-J6
 HC-J8
 HD10-1-25
 HD10-1-3
 BR36-20-164
 BR36-20-166
 BR36-20-165

-A-----G-----TGAG-CT-T-----G-A-TG-CTCTA
 -A-----A-----TGAG-CC-T-----A-G-CTCCA
 -A-----G-----GT-G-T-A-C-A-----G-----G--AG
 -A-----G-----GT-G-T-A-C-A-----G-----G--AG
 -AA---G-----GT-G-T-A-C-A-A-----A--AG
 -AA---G-----GT-G-T-A-C-A-A-----A--AG
 -AA---G-----GT-G-T-A-C-A-A-----A--AG
 -AA---G-----GT-G-T-A-C-A-A-----A--AG

5140
5141
 ACTTACCGTACATCGAGCAAGGGATGCTCGCCGAGCTCAAGCAG
 HCV-1
 HCV-J
 HC-J6
 HC-J8
 HD10-1-25
 HD10-1-3
 BR36-20-164
 BR36-20-166
 BR36-20-165

-C-C-T-----AG-G---CA-CG-A-A-----AT-C-G---TCC
 GAGCGG-TCT---T---G---CA-CG-A-A-----AT-C-G---TCC
 -AGCCG-CCT---T---G---CA-CG-A-G---AT-C---ATCT
 C-GCC---A-----A---CTCA-G-AA-A---C-C-----G--
 C-GCC---A-----A---CTCA-G-AA-A---C-C-----G--
 CTGCC---A---T---A---CTCA-G-AA-A---TC-C-----GGA
 CTGCC---A---T---A---CTCA-G-AA-A---TC-C-----G-A
 CTGCC---A---T---A---CTCA-G-AA-A---TC-C-----G-A
 CTGCC---A---T---A---CTCA-G-AA-A---TC-C-----G-A

Figure 6 • Continued 6

5191	5240	5290
HCV-1	AAGGCCCTGGCCTGCAGACCGCGTCCCCGTCAAGGAGGTTATCGC	CCCTGGCTGCCAGACCAACTGGCAAAACTCGAGACCTTCTGGCGAAGC
HCV-J	-----G-----AT-G-----A--A--CA---AAG--A--G-----C-GCT--	T--C-TG--GG--T----G----G-GCC--T----GT-----A-
HC-J6	-----AT--AA--T-AT-----CAA--T---AAA--A--TC-A-AC--ACA	A--C-----G--TTCT----CC--GG-A---CAA-----C--A-
HC-J8	-----ATA-AA-----A--ACAG--CA-AA-G--A--TC-A-AC--ACA	G--A---A-L---T-ATCA---CC--G--T--ACAA---T----C-A-
HD10-1-25	-----AAT--T--A--G-----CGA--CA---AA--ACA--CT--C--T-A	G--C-TAA--AGCTT-----G--T--A-----CAC-----
HD10-1-3	-----AAT--T--A--G-----CGA--CA---AA--ACA--CT--C--T-A	G--C-TAA--AGCTT-----G--T--A-----CAC-----
BR36-20-164	-----A-T---T--AT-G-----CGA--CA---AA--ACA--CT--C--T-A	G--CATA--AACT-----G--T--G-----CAC-----
BR36-20-166	-----A-T---T--AT-G-----CGA--CA---AA--ACA--CT--C--T-A	G--CATA--AACT-----G--T--G-----CAC-----
BR36-20-165	-----A-T---T--AT-G-----CGA--CA---AA--ACA--CT--C--T-A	G--CATA--AACT-----G--T--G-----CAC-----

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Figure 6 : continued 7

	5292
HCV-1	AT
HCV-J	-C
HC-J6	-C
HC-J8	-C
HD10-1-25	--
HD10-1-3	--
BR36-20-164	--
BR36-20-166	--
BR36-20-165	--

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Figure 7

SEQ ID NO	1290	1300	1310	1320	1330
HCV-1	ITTGSPITYSTYCKFLADGGCGAYDIIICDECHSTDATSIIGIG				
1a	-G-----C-----	-S-T-----			
1b	V---A-----A-----AV-S-T-----				
2a	V---DS-----I-----AA-----V-----T-----				
2b	HC-J8	BE95	270	V-----AS-----Q-----T-----	
5a					
1340	1350	1360	1370	1380	
HCV-1	TVLDQAETAGARLTVVVLATATPPGSVTVPNIEVALSTTGEIPFYGKAI				
1a	I-----I-----N-----				
1b	V---T-----T-----GQE-----R-----				
2a	V-----T-----T-----S-----GHE-----				
2b	HC-J8	BE95	5a	T-----PQE-----V-----R-----	
5a					

SUBSTITUTE SHEET (RULE 26)

Figure 7 - Continued 1

		1390	1400	1410	1420	1430
HCV-1	1a	PLEVIKGGRHLIFCHSKKKCDELAAKLVALGINAVAYYRGLDVSVIPTSG				
HCV-J	1b	-I-A-----	TG--L-----			
HC-J6	2a	--SY-----	A-RGM-L-----	Q-		
HC-J8	2b	--AF-----	A-RGM-V-----	Q-		
BE95	5a	--AF-----	KQ-TS--V-----	A-----A-		
HCV-1	1a	DVVVVATDALMTGYTGFDSVIDCNCNTCVTQTVDFSLDPFTFTIETITLPQD				
HCV-J	1b	F-----F-----	T-----T-----			
HC-J6	2a	F-----VA-----V-----	T-Q-V-----			
HC-J8	2b	-----VA-S-I-----	T-Q-V-----			
BE95	5a	CS-----SA-----	T-V-----			

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Figure 7 . Continued 2

	SEQ	ID	NO	1490	1500	1510	1520	1530
HCV-1	1a			AVSRTQRRGRTGRGKPGIYRFAVAPGERPSGMFDSSVLCECYDAGCAWYEL				
HCV-J	1b			-A-----RS-----T-----				
HC-J6	2a			-S-----RL-----Y-ST-----A-----V-----A-----				
HC-J8	2b			-S-----RL-V-----Y-SS-----V-----A-----				
BE95	5a			-S-----RH-----Y-SA-----D-----V-----D-----				
	SEQ	ID	NO	1540	1550	1560	1570	1580
HCV-1	1a			TPAETTVRLRAYMNTPGLPVCCQDHLEFWEGVFTGLTHIDAHFLLSATKQSG				
HCV-J	1b			-S-----L-----S-----A-----				
HC-J6	2a			-F-----F-----A-----				
HC-J8	2b			-F-----F-----A-----				
BE95	5a			-I-----I-----N-----M-----G-----				
BR36	3a		223	D-----S-----Q-----				

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Figure 7 - Continued 3

		1590	1600	1610	1620	1630
HCV-1	1a	ENLPYLVAYQATVCARAQQAPPSWIDQMWKCLIRLKPTLHGPPTPLLYRLGA				
HCV-J	1b	D-----				
HC-J6	2a	--FA--T-----K-----V-----T-----V-----S-----				
HC-J8	2b	--FA--T-----K-----V-----T-----T-----T-----				
BE95	5a	--F-----V--K-----T-----ML-----T-----P-----				
BR36	3a	L-FST-T-----E-----V-----V-----P-----				
		1640	1650	1660	1670	1680
HCV-1	1a	VQNEITLTHIPVTKYIMTCMSADLEVVTSTWVLVGGVLAALAAAYCLSTGCV				
HCV-J	1b	--V-----I-----A-----				
HC-J6	2a	--T-----V-----A-----Q-----M-----A-----V-----A-----				
HC-J8	2b	--T-----V-----A-----Q-----IM-----S-----A-----V-----A-----I-----				
BE95	5a	--I-----A-----I-----I-----V-----TV-----S-----				
BR36	3a	--C-----I-----A-----T-----L-----V-----V-----				

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Figure 7 - Continued

		1690	1700	1710	1720	1730
HCV-1	1a	VIVGRVV	LSGKPAIIPDREVLYREFDE	MEEC	SQHLPYIEQQGM	LAEQFKQ
HCV-J	1b	- - - I I	- - - R - V - - -	- - - Q - - -	- - - AS - - -	- - - Q - - -
HCV-J6	2a	C - I - L H	VNQRRAVVA -- K --	E A - - -	ASRAAL -- E - QR	I -- ML - S
HCV-J8	2b	S - I - L H	- NDRVVVA -- K - I -	E A - - -	ASKAAL -- E - QR	M -- ML - S
BR36	3a	- - - HIE	- G - - - V - - K - -	Q Q Y - - -	- AA - - - AQV	I - H - - E
BE95	5a	A - - - II	- - - - - A - - Q Q - -	- - - - -	- AS - - - MDETRA	I - G - - E
	NS4-1					
	NS4-5					
	1740				1750	1760
	NS4-7					
HCV-1	1a	K ALGLLQQTASRQA	EVIAPAVQTNWQKLETFWAKH			
HCV-J	1b	- - - - - TK - - -	- AA - - V - ESK - RA - - V - - -			
HCV-J6	2a	- IQ - - - Q - - -	QD - Q - - - AS - P - V - Q - - -			
HCV-J8	2b	- IQ - - - Q - T - -	QD - Q - - - I - SS - P - - - Q - - -			
BR36	3a	- V - - - R - T Q - Q	A -- E - I - T - - - A - - H - -			
BE95	5a	- V -- FIS - TGQK -	- TLK - - ATSV - N - A - Q - - XTY			

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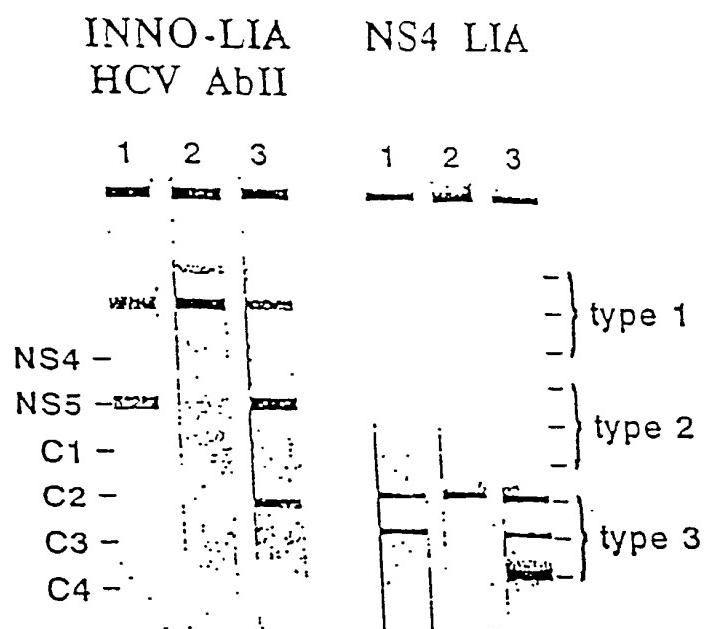


Figure 8

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Figure 9

Figure 9 - Continued 1

Figure 9 - Continued 2

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Figure 9 - Continued 3

301	CGAGGGCTCTGGGCCATTGGGGCCCCAATGACCCCGGGGAATAATCGCGC	400
PC-3-4	- - - - -	
PC-3-8	- - - - -	
PC-2-1	- - - - -	
PC-2-6	- - - - -	
PC C/E1	- - - - -	
351	TAATTTGGGTAAAGGTCAATCGATAACCTAACCGTGGGATTGCCGATCTCA	
PC-3-4	- - - - -	
PC-3-8	- - - - -	
PC-2-1	- - - - -	
PC-2-6	- - - - -	
PC C/E1	- - - - -	

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Figure 9 - Continued 4

SEQ	ID NO	401	TGGGGTATATCCCGCTCGTAGGCCGCCATTGGGGGTGCAGGGCT	450
PC-3-4			-----G-----	
PC-3-8			-----C-----	
PC-2-1			-----	
PC-2-6			-----	
PC-4-1			-----	
PC-4-6			-----	
PC C/E1			-----Y-----	
SEQ	ID NO	451	CTCGCACACGGTGAGGGCCTTGAGGACGGGAAACTATGCAACAGG	500
PC-3-4			-----C-----	
PC-3-8			-----	
PC-2-1			-----	
PC-2-6			-----	
PC-4-1		45	-----	
PC-4-6		46	-----	
PC C/E1			-----S-----	

SUBSTITUTE SHEET (RULE 26)

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Figure 9 - Continued 5

	501	GAATTACCCGGTTGCTCTTCTATCTTATTCTTGCTCTCTCGT	550
PC-3-4		- - - - -	
PC-3-8		- - - - -	
PC-2-1		- - - - -	
PC-2-6		- - - - -	
PC-4-1		- - - - -	
PC-4-6		- - - - -	
PC C/E1		- - - - -	
	551	GTCGTGACCGTTCCGGCCTGCAGTTCACCGAAATGCCCTCTGGGATT	600
PC-3-4		- - - - -	
PC-3-8		- - - - -	
PC-4-1		- - - - -	
PC-4-6		- - - - -	
PC C/E1		- - - - -	

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Figure 9 - Continued 6

601 TATCATGTTACCAATGATTGCCCAAACCTCTCCATAGTCTATGAGGCAGA
PC-3-4
PC-3-8
PC-4-1
PC-4-6
PC C/E1

650
651 TAAACCTGATCCTACACGGCACCTGGTTGGGTGCGCTTGTCGATGACAGGT
PC-3-4
PC-3-8
PC-4-1
PC-4-6
PC C/E1

700

Figure 9 - Continued 7

701 ATGTGAGTAGATGCTGGGTCCAATTACCCCTACACTGTCAGGCCCCGAGC	750 ----- PC-3-4 PC-3-8 PC-4-1 PC-4-6 PC C/E1	800 ----- 751 CTCGGAGGAGTCACGGCTCCCTTGGAGAGGCCGTTGACTACCTAGGGGG	----- PC-3-4 PC-3-8 PC-4-1 PC-4-6 PC C/E1
---	---	--	--

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Figure 9 - Continued 8

801	AGGGGCTGCCCTCTGCTCCGGTTATACGTAGGAGACGGTGTGGGCA	PC-3-4 PC-3-8 PC-4-1 PC-4-6 PC C/E1
851	CTATTCTTGGTAGGCCAAATGTTCACCTATAAGGCCTCGCCAGCACGCTACG	PC-3-4 PC-3-8 PC-4-1 PC-4-6 PC C/E1

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Figure 9 - Continued 9

901
GTGCAGAACTGCAACTGTTCCATTACAGTGGCCATGTACCGGCCACCG
PC-3-4
PC-3-8
PC-4-1
PC-4-6
PC C/E1

SUBSTITUTE SHEET (RULE 26)

950

951
GATGGCA
PC-3-4
PC-3-8
PC-4-1
PC-4-6
PC C/E1

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Figure 10

SEQ ID NO	3856	3890	3940	3990
HCV-1	ACCACTGGCAGCCCCATCACGTACTCCACCTACGG			
HCV-J	--G--G-----TT-			
HC-J6	--G--C--GGCG-----A-T--			
HC-J8	--C--GGA-T-T-----T-T--			
PC1_37	--C--AGCTT-T-----A-----T-----			
C1_48	--C--AGCTT-T-----A-----T-----			
BR36	222	3a		
HCV-1	CAAGTTCCTTGCGGACGGGGGTGCTGGGGGGCTTATGACATAATAA			
HCV-J	--T--A-----C-----C-----C-----C-----C-----C-----			
SUBSTITUTE HC-J6	--A-----C-----T-----G-----C-----G-----C-----C-----			
HC-J8	--TA-C--A--T--A--C--TG-A-CC--T--C-----C-----C-----			
PC1_37	--T--T--A-----T-----A-----C-----GC-----G-G-C-----			
PC1_48	--T--T--A-----T-----A-----C-----G-----G-G-C-----			
BR36	3a			
HCV-1	TTTGTGACGAGTGCCACTCCACGGATGCCACATCCATCTGGCATCGGC			
HCV-J	-A-----T--A-----A--T--CT-G--TA-----			
HC-J6	-A--C--T--A-----TG--GT--CT-T--CA-----TC-C-----A			
HC-J8	-A--C--A-----T--AGT--C--T--TA-----C-T-----T-A			
PC1_37	-A--C-----T--CA-----C-----CA-----TC-T--G-----A-----			
PC1_48	-A--C-----T--CA-----C-----CA-----TC-T--G-----A-----			
BR36	3a			
SUBSTITUTE SHEET (RULE 26)				

Figure 10 - Continued 1

<p>3991 HCV-1 HCV-J HC-J6 HC-J8 PC1-37 PC1-48 BR36</p>	<p>4040 ACTGTCTTGACCAAGCAGAGACTGGGGGGGAGACTGGTTGTCGCG --A---G---T---G---A---C---G---C---C--- --A---C---T---A---C---TC---G---AAC---A---G--- --A---T---C---A---C---TC---G---A---G---TT---G--- --G---G---T---A---T---G---C---C---CT---G--- --G---G---T---A---T---G---C---C---CT---G--- 3a</p>	<p>4041 CACGCCACCCCTCCGGCTCCGTCACTGGCCATCCAAACATCGAGG ---G---A---GA---C---A---C--- T---G---T---G---C---G---A---G---A--- ---A---G---C---TA---G---G---AACT---A--- ---G---C---AGT---G---AAC---C--- ---G---C---AGT---G---AAC---C--- 3a</p>	<p>4091 AGTTGCTCTGTCCACCAAGGAGATCCCTTTACGGCAAGGCTATC -A---G---C---A---T---T---C---C---T---A---C--- ---G---C---CGGGCAGGAG---T---C---C---T---G---G---T--- ---G---C---TGGTCA-GAG---C---T---A---T---A---T--- -A---G---C---TCAGGAG---G---G---T---C---C---GA---C---T--- -A---G---C---TCAGGAG---G---G---T---C---C---GA---C---T--- 3a</p>
<p>SUBSTITUTE SHEET (RULE 26)</p>	<p>4040 HCV-1 HCV-J HC-J6 HC-J8 PC1-37 PC1-48 BR36</p>	<p>4090 HCV-1 HCV-J HC-J6 HC-J8 PC1-37 PC1-48 BR36</p>	<p>4140 HCV-1 HCV-J HC-J6 HC-J8 PC1-37 PC1-48 BR36</p>

Figure 10 - Continued 2

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4141 HCV-1 HCV-J HC-J6 HC-J8 PC1-37 PC1-48 BR3 ⁶	4190 1a 1b 2a 2b 5a 5a 3a	4191 SHCV-1 SUBSTITUTE HC-J6 HC-J8 SHEET PC1-37 PC1-48 (BR3 ⁶)	4240 1a 1b 2a 2b 5a 5a 3a	4241 HCV-1 HCV-J HC-J6 HC-J8 PC1-37 PC1-48 BR3 ⁶	4290 1a 1b 2a 2b 5a 5a 3a
CCCCTCGAAGTAATCAAGGGGGAGACATCTCATCTGTCTGCATTCAAA ---A-T---G-CC--- ---GTC-TAC--- ---A-CTT-C--- ---T-CTT-T-A--- ---T-CTT-T-A--- ---T-CTT-T-A--- ---T-CTT-T-A--- GAAGAAGTGGGACGGAAACTCGCCGCAAAGCTGGTCGCATTGGGCATCAATG ---T---G--- ---A---T---G--- ---G--- ---A---A---T---T--- ---A---A---T---T--- ---A---A---T---T--- CCGTGGCTACTACCCGGTCTTGACGTTCCCGTCAATCCCGACCAGCGGC -T--A--G--T--- -A--A--A--G--G--- -T--A--TA-G--- ---A--T--TA-A--- ---A--T--TA-A--- (RULE 26)					

Figure 10 - Continued 3

HCV-1 HCV-J HC-J6 HC-J8 PC1-37 PC1-48 BR36	1a 1b 2a 2b 5a 5a 3a	4291 GATGTTGTCGTGGCAACCGATGCCCTCATGACCGGCTATACCGGCGA --C--C--T-----A--C--T--A-----G--T--T----- --C--A--G----C--C--C-----G--G--T--T--A-- --C--G--G--T--C--C--T-----A-----T--G--C-- --C--G----GTGCAGC-----C--G-----G--A--TC-- --C--G----GTGCAGC-----C--G-----G--A--TC-- 3a	4340 4390	4341 CTTGACTCGGTGATAGACTGCAATACTGCTGTCACCCAGACAGTCGATT ---T----A----C----C----A---- ---T----C----C----C----A---- ---T----C----C----C----C---- ---T----C----C----T----AGTT--A--C-- ---T----C----C----T----T----T--T--C-- ---T----T----C----T----T----T----G--C-- ---T----T----C----T----T----G----C-- ---T----T----C----T----T----G----G--C-- 3a	4391 TCAGCCTTGACCCCTACCTTACCATTGAGACAATCACGCTCCCCAGGAT ---T-G--T-C-----G-CA---G-----A--C ---T-G--C-A-----AACC--CAG--TG---T-A--C ---A-----A-----CACC--TCAA--CG---T---C ---T-G--T-C-T-----T-C----AG-G-----C ---T-G--T-C-T-----T-C----AG-G-----C 3a	4440
HCV-1 HCV-J HC-J6 HC-J8 PC1-37 PC1-48 BR36	1a 1b 2a 2b 5a 5a 3a					

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Figure 10 - Continued 4

			4490
HCV-1	1a	GCTGTCTCCGCACCTCAACCGTGGGGCAGGACTGGCAGGGAAAGCCAGG	
HCV-J	1b	--G--G--G--TG-G--G--A--T-----C-G-A GT--	
HC-J6	2a	--A--T-GC--G--C-----C-C-G-----A-GA-TG--	
HC-J8	2b	--T G-----A-A-G-----G-----CGATTG--	
PC1_37	5a	--A--G--A-A-GC--G-----T-----C-C-G-----A--T-G--AC--	
PC1_48	5a	--A--G--A-A-GC--G-----A-----C-C-G-----A--T-G--AC--	
BR36	3a		
			4491
HCV-1	1a	CATCTACAGATTGTGGCACCGGGGAGGCCCTCCGGCATGTTGACT	
HCV-J	1b	--G-----A-T--A--A--G-----A-----	
HC-J6	2a	T--T--T--G-A--TT-CA-T--T-----A-----T--A	
HC-J8	2b	-G-T-----G-A--TT-GT-A--C-----A-G--G-----A	
PC1_37	5a	--A---C-G-A---CT-GG-T--A---A-A--G-----	
PC1_48	5a	--A---C-G-A---CT-GG-T--A---A-A--N---T-A-----	
BR36	3a		
			4550
SUBSTITUTE SHEET (RULE 26)			
HCV-1	1a		
HCV-J	1b		
HC-J6	2a		
HC-J8	2b		
PC1_37	5a		
PC1_48	5a		
BR36	3a		
			4551
HCV-1	1a	CGTCCGTCCTCTGTGAGTCCTATGACGCAGGGCTGTGCTATGAGCTC	
HCV-J	1b	-C-G-----G-----C-----	
HC-J6	2a	GTGTA--G-----C-----C-T-----GGCC-----A-----	
HC-J8	2b	GCGTA--G-----C-----T-----C-----C-----C-----T	
PC1_37	5a	-CGTG--G-----C-----T-----C-----A-----C-----T-----G	
PC1_48	5a	-CGTG--G-----C-----T-----C-----A-----G-----T-----G	
BR36	3a		

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Figure 10 - Continued 5

			4591	ACGCCCGCCGAGACTACAGTTAGGCTACGGAGCGTACATGAACACCCCCGGG
HCV-1	1a			- - - - - T - - - CT - G - - - T - G - - G - - T - - C - A - - T - - A - -
HCV-J	1b			- - - A - - A - - G - - - C - - C - - CA - - A - - TT - C - - A - - T - -
HC-J6	2a			- - A - - T - - T - - - G - - A - - C - - G - - T - - TT - C - - G - - C - -
HC-J8	2b			- - T - - T - - - C - - G - - T - G - - C - - T - - N - A - - - C - -
PC1-37	5a			- - T - - T - - - C - - G - - T - G - - C - - T - - A - - - C - -
PC1-48	5a			
BR36	3a			
			4640	
HCV-1	1a			
HCV-J	1b			
HC-J6	2a			
HC-J8	2b			
PC1-37	5a			
PC1-48	5a			
BR36	3a			
			4641	GCTTCCCGTGTGCCAGGACCATCTTGAATTGGAGGGCGTCTTACAG
HCV-1	1a			- T - G - - - C - - - A - - G - - C - - - A - - C - - -
HCV-J	1b			- TT - G - - T - - - A - - - G - - - CA - - T - - C - - C - -
HC-J6	2a			- TT - G - - A - - T - - - C - - G - - G - - A - CG - - -
HC-J8	2b			- - C - - T - - C - - T - - - T - G - - - C - - G - - C - G - -
PC1-37	5a			- - C - - T - - C - - T - - - T - G - - - C - - G - - C - G - -
PC1-48	5a			
BR36	3a			
			4690	
HCV-1	1a			
HCV-J	1b			
HC-J6	2a			
HC-J8	2b			
PC1-37	5a			
PC1-48	5a			
BR36	3a			
			4740	
HCV-1	1a			
HCV-J	1b			
HC-J6	2a			
HC-J8	2b			
PC1-37	5a			
PC1-48	5a			
BR36	3a			
			4691	GCTCTCACTCATATAGATGCCCACTTCTATCCCAGACAAAGCAGAGTGGG
HCV-1	1a			- - - C - - C - - - C - - T - - - C - - A - - GCA - - A
HCV-J	1b			- - - A - - C - - - A - - C - - T - - - A - - - ATCG - - -
HC-J6	2a			- T - - A - - C - - T - - C - - C - - C - - G - - AG - A - A
HC-J8	2b			- G - - - A - C - - C - - C - - T - - A - G - - A - - C - - A - - G - -
PC1-37	5a			- G - - - A - C - - C - - T - - A - G - - G - - A - - C - - A - - G - -
PC1-48	5a			
BR36	3a			

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Figure 10 - Continued 6

		4790
HCV-1	1a	GAGAACCTTCCTTACCTGGTAGCGTACCAAGCCACCGTAGGGC
HCV-J	1b	--C---C---C---A-----A-----A-----C-----
HC-J6	2a	--A--TT-CG-A---T-PAC---C---G---T---A-----
HC-J8	2b	--A---T---G-G---T---AACG---C---G---A---A-----
PC1-37	5a	--TT-C---A---T-----A---A---C---T-T-C-C---
PC1-48	5a	--TT-N---A---T-----A---A---C---T-T-C-C---
BR36	3a	CTC---T-CT-G-T---ACT---C-----T-----C-C---
		4791
HCV-1	1a	TCAAAGCCCCCTCCCCATCGTGGGACCAAGATGTGAAAGTGTGATTGCGC
HCV-J	1b	--G---T---A---T-----A-----C-C---A---G-----
HC-J6	2a	CA---C---G---C-----GTC-----C---A-----
HC-J8	2b	AA---G---T---T-----GT-----C-A-C-A-G-----
PC1-37	5a	GA---G---C-----ACA-----A---CA---C-C---T-----
PC1-48	5a	GA---G---C-----ACA-----A---CA---C-C---T-----
BR36	3a	G---G---T-----AGT-----G-----C-CG-A---G-----
		4840
HCV-1	1a	TCAAAGCCCCCTCCATGGGCCAACACCCCTGCTATACAGACTGGGGCT
HCV-J	1b	--A---A---G-----G-----G-----G-----A---A---C-----
HC-J6	2a	--A---GTG---C---C-----T---C---G---A---A---C-----
HC-J8	2b	--A---T---A---GAC---T---C---G---C---CT-----T---C-----
PC1-37	5a	--A---G---NT-AAC---C---T---T-----G-----GC-C-----
PC1-48	5a	--A---G---TT-AAC---C---T---T-----CT-G-----G-----GC-C-----
BR36	3a	-T---A---A---A---A---T---G---T---T-----TC-GT-----GC-----
		4890
HCV-1	1a	TCAAAGCCCCCTCCATGGGCCAACACCCCTGCTATACAGACTGGGGCT
HCV-J	1b	--A---A---G-----G-----G-----G-----G-----A---A---C-----
HC-J6	2a	--A---GTG---C---C-----T---C---G---C---CT-----T---C-----
HC-J8	2b	--A---T---A---GAC---T---C---G---C---CT-----T---C-----
PC1-37	5a	--A---G---NT-AAC---C---T---T-----G-----GC-C-----
PC1-48	5a	--A---G---TT-AAC---C---T---T-----CT-G-----G-----GC-C-----
BR36	3a	-T---A---A---A---A---T---G---T---T-----TC-GT-----GC-----

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Figure 10 - Continued 7

		4891	GTT CAGAATGAAATCACCCCTGACGGACCCAGTCACCAAATCATCATGAC
HCV-1	1a		- - - A - - - GG - - - T - - C - - A - - - CA - - - G - -
HCV-J	1b		- - - A - - - GG - - - T - - C - - A - - - CA - - - G - -
HC-J6	2a		- - - ACC - - C - - GG - - - C - - - T - - T - - G - - - GCC - -
HC-J8	2b		- - - GACC - - - GG - - - T - - - C - - G - - - G - - - GCC - -
PC1-37	5a		- - C - - - G - - - A - - - CA - - - G - - - T - - G - -
PC1-48	5a		- - C - - N - - G - - - A - - - CA - - - G - - - T - - G - -
BR36	3a		- - C - - A - - - TG - T - - A - - - CA - - - A - - - G - -
		4940	
HCV-1	1a		
HCV-J	1b		
HC-J6	2a		
HC-J8	2b		
PC1-37	5a		
PC1-48	5a		
BR36	3a		
		4941	ATGCATGTCGGCGGACCTGGAGGT CGTCA CGAGCACCTGGGTGCTCGTTG
HCV-1	1a		- - - - - T - - - - - T - - - - - T - - - - - A - - - A - -
HCV-J	1b		- - - - - T - - - - - T - - - - - T - - - - - A - - - A - -
HC-J6	2a		- - - CAA - - - - - T - - - - - A - - - G - - - C - - - CT - A - C - -
HC-J8	2b		- - - CAA - - T - - - C - - A - - A - - G - - A - - T - A - - C - - G - - CG - -
PC1-37	5a		- - - T - - - G - - - T - - - A - T - - C - - - T - - - T - - G - - G - -
PC1-48	5a		- - - T - - - G - - - T - - - A - T - - C - N - - T - - - T - - G - - G - -
BR36	3a		- - - A - - T - - T - - - A - - AAC - - C - - - TT - GC - - -
		4991	CGGGCGTCTGGCTTGCTTGGCCGGTAT TGCCTGCAACAGGCTGGCGTG
HCV-1	1a		- - - A - - - T - - G - - - C - - - C - - - A - - - A - - -
HCV-J	1b		- - - G - - - T - - - G - - CG - C - - - C - - - G - - C - - G - - T - - T
HC-J6	2a		- - - G - - G - - A - - C - - CG - - A - - T - - C - - - G - - T - - - A - T
HC-J8	2b		- - - G - - - TG - - - G - - CC - - - G - - C - - T - - A - GGTG - - T - CG - - A
PC1-37	5a		- - - G - - - TG - - - G - - CC - - - G - - C - - T - - A - GGTG - - T - CG - - A
PC1-48	5a		- - - A - - - G - - - CC - - - G - - C - - T - - A - GGTG - - T - CG - - A
BR36	3a		- - - A - - - G - - - C - - - G - - C - - T - - - T - - T
		5040	
HCV-1	1a		
HCV-J	1b		
HC-J6	2a		
HC-J8	2b		
PC1-37	5a		
PC1-48	5a		
BR36	3a		

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Figure 10 - Continued 8

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Figure 10 - Continued 9

			5191	AAGGCCCTCGGCCTCTGCAGACCGCGTCCCGTCAGGAGGGTATCGC
HCV-1	1a	--G----AT-G----A--CA--AAG--A--G----C-GCT--		
HCV-J	1b	--AT--AA---T-AT---CAA---T---AAA---A---TC-A-AC--ACA		
HC-J6	2a	--ATA-AA----A--ACAG--CA-AA-G--A--TC-A-AC--ACA		
HC-J8	2b	--A-TG----T--A-CAGC--GA-CGG--AGA---T--AAC-C-GAA		
PC1_37	5a	--A-TG----T--A-CAGC--GA-CGG--AGA---T--AAC-C-GAA		
PC1_48	5a	--A-T----T--AT-G----CGA--CA---AA--ACA--CT--C--T-A		
BR36	3a	--A-T----T--AT-G----CGA--CA---AA--ACA--CT--C--T-A		
			5240	
			5290	
HCV-1	1a	CCCCTGCTGTCCAGACCAACTGGCAAAACTCGAGACCTCTGGCGAAGC		
HCV-J	1b	T--C-TG--GG--T----G----G-GCC--T----GT----A-		
HC-J6	2a	A--C----G----G-TTCTT----CC--GG-A--CAA--C--A-		
HC-J8	2b	G--A--A-A--T-ATCA----CC--G--T--ACAA--T----C--A-		
PC1_37	5a	G--G--A-C-AC-T-TGTG--A-C--GGCT--CAG--N-C-CAT		
PC1_48	5a	G--G--A-C-AC-T-TGTG--A-C--GGCT--CAG--C-CAT		
BR36	3a	G--CATA--AACT-----G--T----CAC-----		
			5241	
HCV-1	1a	CCCCTGCTGTCCAGACCAACTGGCAAAACTCGAGACCTCTGGCGAAGC		
HCV-J	1b	T--C-TG--GG--T----G----G-GCC--T----GT----A-		
HC-J6	2a	A--C----G----G-TTCTT----CC--GG-A--CAA--C--A-		
HC-J8	2b	G--A--A-A--T-ATCA----CC--G--T--ACAA--T----C--A-		
PC1_37	5a	G--G--A-C-AC-T-TGTG--A-C--GGCT--CAG--N-C-CAT		
PC1_48	5a	G--G--A-C-AC-T-TGTG--A-C--GGCT--CAG--C-CAT		
BR36	3a	G--CATA--AACT-----G--T----CAC-----		
			5291	
HCV-1	1a	AT		
HCV-J	1b	-C		
HC-J6	2a	-C		
HC-J8	2b	-C		
PC1_37	5a	-C		
PC1_48	5a	-C		
BR36	3a	--		

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Figure 11

	SEQ ID NO
HCV-1	1286
	T TG S P I T Y S T Y G K F L A D G G C S G G A Y D I I I C D E C H S T D A T S I L G I G T V L D Q A E T A G A R L V V
HCV-J	- - G - - - C - - -
HC-J6	- - A - - - A - - -
HC-J8	- - D S - - - I - - -
PC-1-48	- - A S - - - V - - -
PC-1-37	- - A S - - - H - V - -
	S - T - - - -
	A V - S - T - - -
	V - - T - - - -
	56
	58
HCV-1	1346
	L A T A T P P G S V T V P H P N I E E V A L S T T G E I P F Y G K A I P L E V I K G G R H L I F C H I S K K C D E L A A
HCV-J	- - I - - - N - - -
HC-J6	- - T - - - G Q E - - -
HC-J8	- - T - - - S - - -
PC-1-48	- X - - - T - - -
PC-1-37	- X - - - T - - -
	I - A - - - -
	R - - S Y - - -
	A F - - - -
	N - - - -

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Figure 11 - Continued 1

1406	KLVALCINAVAYYRGLDVSIVIPTSGDVVVVATDALMTGYTGDFDSVIDCNTCVTQTVDFS	
HCV-1	- - TG - - L - -	F - - -
HCV-J	- - RGM - - L - -	F - - -
HC-J6	Q - -	V - - -
HC-J8	Q - -	VA - - -
		VA - - S - I - -
1466	LDPTFTIETITLPQDAVSRTQRGGRTGRGKPGIYRFVAPGERPSGMFDSSVLCCECYDAGC	
HCV-1	- - T - - A - -	T - - -
HCV-J	- - T - Q - V - -	RS - - -
HC-J6	S - -	A - - -
HC-J8	T - Q - V - -	RL - Y - ST - -
		V - - -
1526	AWYELTPAETTVRLRAYMNTPGLPVCQDHILEFWEGVFTGLTHIDAHFLSQTKQSGENLPHY	
HCV-1	- - S - - - L - -	S - - -
HCV-J	- - F - -	A - - -
HC-J6	A - -	G - - -
HC-J8	F - -	FA - - -

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Figure 11 - Continued

1586 HCV-1 LVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLYRLGAVQNEITLTHPVTKYI
HCV-J -----
HCV-J6 -T-----K-----V-----T-----V-----
HC-J8 -T-----K-----V-----T-----V-----

1646 MTCMSADLEVVTSTWVLLGGVLAALAAAYCLSTGCVVIVGRVVVLSGKPAIIPDREVLYREF
 HCV-1 -A-----T-S-----I-I---R---V---Q---
 HCV-J A----Q----M----A----V----A----C-I---LHVNQRAVVA---K---EA---
 HC-J6 A----Q----IM---S----A----V----A----IS-I---LH-NDRVVVA---K---I---EA---
 HC-J8 A----Q----I-X----V-X----TV-S-A---I-I---A---XQ---
 PC-1-48 -A----I-X----V-T-XX---TV-S-A---I-I---X---QQ---
 PC-1-37 -AF---P---I-X----V-T-XX---TV-S-A---I-I---X---QQ---

1706
 HCV-1 DEMEECSQHLPYIEQGMMMLAEQFKQKALGLLQTA
 HCV-J -----
 HC-J6 -----
 HC-J8 -----
 PC-1-48 AS--
 PC-1-37 AS--
 TK-- AA-- V- ESK- RA-- V-
 Q-- K- QD- Q-- AS- P- V- Q-
 E- QRI- ML- S- IQ- Q- T- QD- Q- I- SS- P- Q-
 E- QRM- ML- S- IQ- Q- FIS- TGQK- TLK- ATSV- N- AXQ- - TY
 MDET RAI- G- E- V- FIS- TGQK- TLK- ATSV- N- ADQ- XTY
 MDET RXI- G- E- V- FIS- TGQK- TLK- ATSV- N- ADQ- XTY

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Figure 12

HCV1 HCVJ HCJ6 HCJ8 NZL1 HCVTR BE95	1a 1b 2a 2b 3a 3b 5a	330 340 350 360 370	PTTALVMAQLLRIPQAILDMIAGAHHWGVLAGIAYFSMVGNNWAKVLVVLLL ---VS---VV---V----- --ATMIL-YAM-V-EV-I-I-G-----MF-L-----Q-A----V-I--- --LTMI-L-YAA-V-ELV-EI-F-G-----VF-L-----Q-A----IAI--- -AVGM-V-HV--L--TLF-IM-----I---L--Y---Q----AIIMVM --IG--ISH-M-L--TLF-LVST-----M---L---Q----VI--IM ---LV---VVI-I---S---FAA--YAS-A--T--VL--F-
HCV1 HCVJ HCJ6 HCJ8 NZL1 HCVTR BE95	1a 1b 2a 2b 3a 3b 5a	380 390 400 410 420	E2 FAGVDA ETHVTGGSAIGHTVSGFVSSLAPGAKQNQVLINTNGSWHLNSTAL ---G H-----RVAASSTQSL--W-SQ-PS-KI--V-----I-R--- ---A Q---TV---TA-NARTLTGMFSL--R-KI-----I-R--- ---V T-YSS-QE--R--A--AG-FTT-----LY-----I-R--- ---S H-YT---T-SRHITQA-AG-FDI-PQ-KL--V-----I--- ---S N-YT-A--MAQSIIYRLTDIFST-PS-KL--V-S--- ---T-QIS---SAQ-TY-IA-FITR--Q-KL-----I-R---

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Figure 12 - Continued 1

		430	440	450	460	470	*
		-*	*	-	-	*	*
HCV1	1a	NCNDSSLNTGWLAGLFYHHKFNSSGC PERLASCRPLTDFDQGWGPISY AN					
HCVJ	1b	-Q--FI-A---A-R-A-----M-----IDE-A-----TH DM					
HCJ6	2a	-H--F--S---T-S-----MSA--SIEA-RV---ALQ-ED-					
HCJ8	2b	-Q--F--S---T-----S-----G-D--RI--TLE-ET-					
NZL1	3a	-E-I---FI-----Y-----T---Q---S---K-I-F-R----LTD--					
HCVTR	3b	-Q--FI-----Y-----D-M---A-AT-----T---					
BE95	5a						
		480	490	500	510	520	
		-	-	-	-	-	
HCV1	1a	GSGP/DQRPYCWHYPPKPCGIVPAKSVCGPVYCFTPSPVVGGTTDRSGAP					
HCVJ	1b	PESS/-A-R---SQ-----F--					
HCJ6	2a	VTN-E-M-----RQ--V-S-S-----L--					
HCJ8	2b	VTNDG-M-----R-----RT-----KQ-V-					
NZL1	3a	IT--S-D-----A-R--D---S--					
HCVTR	3b	I---S-DK-----R--V--QE-----SK-H-					
BE95	5a						

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Figure 12 - Continued 2

	530	540
	*	
HCV1	TYSGENDTDVFVLNTRPPL	
HCVJ	--E---	--LL--TRP-QG
HCJ6	--T---E---	--L--S----Q
HCJ8	--T---E---	--L--S----R
NZL1		
HCVTR		
BE95		
1a		--N--S-V--F-LM-----I
1b		
2a		
2b		
3a		
3b		
5a		

Figure 13

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Figure 13 - Continued

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Figure 13 - Continued 2

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Figure 13 - Continued 3

1130
 TATTGCCCCGGTGCACGGAAACCCACAGTCACCGGGGAAGTGGCGGC

HCV-1	1a	1a	-G-	-C-	-T-	-AT-	-T-	-CAA-	-C-
HCH-H	1a	1a	-C-	-T-	-T-	-G-C-C-	-G-A-	-G-TA-C-	
HC-J1	1a	1b	-T-	-T-	-T-	-G-G-T-	-G-A-	-GGCGCAA-C-	
HCV-J	1b	1b	-C-	-C-	-T-	-G-G-T-	-ACGT-G-	-GGCG-A-	
HCV-BK	1b	1b	-C-	-C-	-T-	-G-CG-T-	-ACGT-G-	-GGTG-	
HC-J4 . 83	1b	1b	-C-	-C-	-T-	-G-TC-TT-	-ACG-A-	-GTCGCAA-CT	
HC-J4 . 91	1b	1b	-C-	-C-	-T-	-G-TC-TT-	-ACG-A-	-GTCGCAA-CT	
HCV-JTA	1b	1b	-C-	-C-	-T-	-T-G-T-	-CGT-T-	-GGCGAG-	
HCV-JTB	1b	1b	-C-	-C-	-T-	-T-G-T-	-CGT-T-	-GGCGAG-	
HCV-CHINA	1b	1b	-T-	-T-	-T-	-G-AGT-AT-	-GT-A-A-	-G-CA-TG-C-	
HCV-T	1b	1b	-C-	-C-	-T-	-G-ACT-T-	-GT-A-T-	-GCA-AA-	
HCV-JK1	1b	1b	-C-	-C-	-T-	-GAACC-T-	-G-A-	-GGCGCAA-T	
HCUNK	1b	1b	-T-	-T-	-T-	-G-C-C-	-T-ACA-G-	-GCAC-T-C-	
HCV-N	2a	2a	-GGCC-	-G-	-C-	-TAC-GTT-	-TTC-A-	-CG	
HC-J6	2b	2b	-TG-	-G-	-G-	-AACCT-	-T-TTC-G-	-CCAGGAA-G-T	
HC-J8	2a	2a	-GCC-	-T-	-A-	-G-T-	-AGC-A-	-G-ATCT	
HC-J5	2b	2b	-TG-C-	-A-	-A-	-G-T-	-G-AC-GTT-C-	-T-CG	
HC-J7	3a	3a	-G-CT-A-	-G-	-G-	-CC-C-	-AT-TAC-A-	-T-C-C-ATCT	
NZL1	3a	3a	-C-	-T-A-	-G-	-T-C-	-AT-TAC-	-T-C-C-TG-CT'	
HEM26	3a	3a	-C-	-T-A-	-G-	-T-C-	-A-G-A-	-C-C-A-CT'	
TH85	3a	3a	-G-	-T-A-	-G-	-T-C-	-CAGG-A-TA-	-CTC-ATG-CT	
US114	5a	5a	-G-	-A-	-G-	-T-TACT-	-GA-TT-G-C-	-CTCCAG-C-	
BE95									

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Figure 13 - Continued 4

		1180
		CACACTGTGTCCTGGATTAGCCCTCGCACAGGCCAAGCAGAA
HCV-1	1a	-G---CAC-G---GC---G-T---TA---
HCHI-H	1a	-G-G-CA---C---T-A---T-
HC-J1	1a	TC---GCACCCAGA-CC-C-GTC-TGG---T---A---C-ATCT-
HCV-J	1b	A-A---CACCAACA-GC-C-GTC-A-GT---AGT---GC-GTCT-
HCV-BK	1b	--CACC---CACGC-C-CGTC---T---T---G---GTCT---G
HC-J4 . 83	1b	-G---CACCC-C-G---CACGTC---T---T---T---T---G---GTCT---G
HC-J4 . 91	1b	-G---CACACCCAGA-CG-CACGTC-T---T---A-C-A---GC-GGCC---G
HCV-JTA	1b	-G---CACACCCAG-GG-C-CGTC-T---T---A-C---GC-GGCC---G
HCV-JTB	1b	-G-T-CACCCCTC-G---CACGTC---T---TA---T---G---TCT---G
HCV-CHIINA	1b	-G---CACCCACA-TC-C-CGTCCT---T---TA---A---G-GTCC---G
HCV-T	1b	-G---CACCCGGC-CG---CGTC-T---T---AGT---T---T-GGCT---G
HCV-JK1	1b	-GGG-C-CTAGCTGG-AACGTC---T---TAGC---T---GC-GGTT---C-C
HCUNK	1b	-GTCACCAGC-G---CGG---T---TA---T---GC-GTCT---G
HCV-N	1b	-T-AC-CCAGGAGCCC-CACCG---A-GT---T-C-CTT---T---G---G
HC-J6	2a	-GT---C---CG-G---G---C-C-G---T---TA-TA-T---T---G
HC-J8	2b	GCA---CACCAAGG-C---CACC---A-GT---T-CV-T---T-G---G
HC-J5	2a	--T---C---TAGA---G-C-CC---A-T---AGC---T---T-CG---G
HC-J7	2b	-GTCA-ACCCAA-CG---C-G-T---TT-T-ACAT---C---C-A---C
NZL1	3a	-TG---ACCAGA-GA-A-C---T---TT-TA-TGTG---CGC---G
HEM26	3a	--TGA---C-ACA-G---C---TT---AAT-GG---CGA---A---A
TH85	3a	-GTGA---C-ACA-G---CAC-G---T-CT---C-GG---C---GT---G
US114	3a	-A---GAC---A---CA-C-CCTCAT-TA---A-C-GC---GC---G
BE95	5a	

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Figure 13 - Continued

1230		CGTCCAGCTGATCAACACCAAACGGCAGTTGGCACCTCAATAGCACGGCCC	
HCV-1	1a	-A-----	A-----
HCH-H	1a	-A-----	A-----
HC-J1	1a	-A-----	A-----
HCV-J	1b	AA----A-CG-G-	C-----
HCV-BK	1b	AA----T-A-----	T-G-----
HC-J4.8	1b	AA----TG-G-T-----	C-----
HC-J4.9	1b	AA----TG-G-T-----	C-----
HCV-JTA	1b	AA----C-A-----	T-----
HCV-JTB	1b	AA----C-A-----	T-----
HCV-CHINA	1b	GA----T-A-----	T-----
HCV-T	1b	AA----T-A-----	T-----
HCV-JK1	1b	AA----A-TG-T-----	A-----
HCUNK	1b	-C-----C-A-----	C-----
HCV-N	1b	AA----T-A-----	T-----
HC-J6	2a	AA----C-----	T-----
HC-J8	2b	-C----T-TT-A-----	T-----
HC-J5	2a	-C-T-----C-T-----	T-----
HC-J7	2b	TA--AGT--A-----	T-----
NZL1	3a	AC-G-----G-----	T-----
HEM26	3a	AC-G-----G-----	T-----
TH85	3a	-C-G---T-G-----	T-----
US114	3a	-C-G---G-----	T-----
BE95	5a	AC-G---C-A-----	A-----

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Figure 13 - Continued

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Figure 13 - Continued 7

1330
CACCACAAAGTTCAACTCTCAGGCTGTCCTAGAGGGCTAGCCAGCTGCCG

HCV-1	1a	--G----A----	G-----	C-----T-G-----
HCH-H	1a	--A----A----	G-G--C-C-G-----	C-CA-G-T-----
HC-J1	1a	--G-----	C-G-C-G-----	C-CA-G-CAG-----
HCV-J	1b	GCA-----	G-C-G-C-----	C-CA-G-CAG-----
HCV-BK	1b	ACA--T-GT-----	G-C-G-C-----	C-CA-G-CAG-----
HC-J4 . 83	1b	ACA--G-----	G-C-G-C-----	C-CA-G-CAG-----
HC-J4 . 91	1b	ACA-----	G-C-A-C-----	C-CA-G-CAG-----A-
HCV-JTA	1b	GCA-----	G-C-A-C-----	C-CA-G-CAG-----A-
HCV-JTB	1b	GCA-----	G-G-C-A-----	C-CA-G-CAG-----
HCV-CHINA	1b	ACA--G-----	G-G-C-G-----	C-CA-G-CAG-----
HCV-T	1b	GCG-----	G-G-C-G-----	C-CA-G-CAG-----
HCV-JK1	1b	GTAAG-----	G-G-C-G-----	C-CA-G-CAG-----
A-AT--G-----	A-AT--G-----	A-AT-----	A-CT-A-----	T-----T-----
HCUNK	1b	A-CAT--G-----	G-C-A-----	C-CA-G-CAG-----
HCV-N	1b	AC--GC-----	G-A-----	C-CA-G-T-----T-----
HC-J6	2a	AC-----	AGC-----	T-----C-----C-CT-G-----CG-----
HC-J8	2b	GT-A--CGC-----	T-G-----	A-----C-----C-CT-G-----GT-----
HC-J5	2a	GT-AGACGT-----	AGC-----	T-----C-----C-CT-GT-----TTC-----
HC-J7	2b	T-----T-----	A-T-----A-----	C-----C-----C-CT-GT-----TTC-----
NZL1	3a	T-T--T-----	A-T-----A-----	C-----C-----C-CT-GT-----TTC-----
HEM26	3a	T-----T-----	A-T-----A-----	C-----C-----C-CT-GT-----TTC-----
TH85	3a	T-TA-T-----	A-T-----A-----	C-----C-----C-CA-CAG-----T-----AA-----
US114	3a	T-----T-----	A-G-----T-----	C-----C-----C-CA-CAG-----T-----AA-----
BE95	5a	T-----T-----	T-----A-----	C-----C-----C-CA-CAG-----T-----AA-----

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Figure 13 - Continued 8

		1380	ACCCCTTACCGATTGACCAGGGCTGGGCCCTATCAGTTAT
1a	HCV-1	-G-	T-----
1a	HCH-H	-G-	C-----
1a	HC-J1	-G-	G-----
1b	HCV-J	C--A-CGAT-----	G-----
1b	HCV-BK	C-----A-G-----	T-----C-----
1b	HC-J4 . 83	C-----A-GA-TGG-----	A-----
1b	HC-J4 . 91	C-----A-GG-----	C-----A-----
1b	HCV-JTA	CT-----A-CGA-----	A-----
1b	HCV-JTB	CT-----A-GA-----	T-----C-----
1b	HCV-CHINA	C-----A-GATACA-----	C-----
1b	HCV-T	TT-----A-GA-----	A-----T-----
1b	HCV-JK1	T-----A-GA-AGG-----	T-----C-----
1b	HCUNK	C-----A-GATACA-----	C-----
1b	HCV-N	CT-----A-GA-----	A-----
2a	HC-J6	CAGTA-CGAG-----	G-----CT-----ACAA-----GAG-A-----
2b	HC-J8	CGGG-----GGA-----	AA-CCT-GGAA-----CGAAA-----
2a	HC-J5	CAG-A-CGAG-----	A-CCT-GCAA-----CGAG-AT-----
2b	HC-J7	TAAG-GGAT-----	AA-CCT-GGAA-----GAGA-----
3a	NZL1	G-----A-C-TTTC-----	CT-A-CAG-----T-----
3a	HEM26	G-----A-C-TTCC-----	CT-G-CAG-----AA-----
3a	TH85	G-----A-C-TGCC-----	CT-G-CAG-----T-----
3a	US114	G-----A-C-TGCC-----	G-----T-----C-----
5a	BE95	GG-----G-----AC-----	AA-----C-----

Figure 13 - Continued 9

1430 GACCAGCCCCCTACTGGCACTACCCCCCA

HCV-1	1a	ACGGAAAGGGGGCC	T-----	G-A-----	-T-----	G-G-T
HCH-H	1a	TGCGCTGAGA-T-G	A-----	A-G-A-T-----	A-----	A-T
HC-J1	1a	-GTCT---A-AT-A	-----	-----	T-----	G-G-T
HCV-J	1b	-GCCCTGA-A-G	T-----	A-G-T-----	T-----	G-G-T
HCV-BK	1b	-GCCCT-A-A-G	T-----	A-G-T-----	T-----	G-A-T
HC-J4-83	1b	-GCCCT-A-A-G	T-----	A-G-T-----	T-----	G-A-T
HC-J4-91	1b	-GCCCT--G-A-TG	T-----	A-G-T-----	T-----	G-G-T
HCV-JTA	1b	-GCCCTG-G-A-TTG	T-----	A-G-T-----	T-----	G-A-C
HCV-JTB	1b	-GCCCTGATA-T-G	T-----	A-G-T-----	T-----	G-A-T
HCV-CHINA	1b	-G-CTGA-AT--AG	-----	-----	-----	-----
HCV-T	1b	-GTCTC--A-T-G	-----	AA-G-T-----	-----	G-G-T
HCV-JK1	1b	-GCCTCAT-ATTG	T-----	A-G-T-----	-----	-----
HCUNK	1b	-TCCT-AA-A-G	-----	A-G-T-----	-----	-----
HCV-N	1b	-T-TC-C-AAT--AGAG-	TAT-A-A-G-T-----	-----	-----	G
HC-J6	2a	--TC-C-AA-GATGGG--	AT-A-G-G-----	-----	-----	A-----
HC-J8	2b	-T-TC-C-AAT--AGAA-	TAT-A-A-G-----	-----	-----	G-----
HC-J5	2a	-T-TT-C-AA-GAGGAG--	AT-A-A-G-----	-----	-----	G-A-T
HC-J7	2b	-ATC-C---T-TTCT--TG-CA-A-A-----	-----	-----	-----	G-A-T
NZL1	3a	-ATCTC---TT-GTCC--AG-CAAA--G-----	-----	-----	-----	G-A-T
HEM26	3a	--ATC-C---T-TCT--TG-CAAA--A-----	-----	-----	-----	G-A-T
TH85	3a	--ATC-C---ATT-TTCT--TG-CAAA--G-----	-----	-----	-----	T-----
US114	3a	--ATP-TCG---T---AGT---TG-CAAA--A-T-----	-----	-----	-----	-----
BE95	5a	-----	-----	-----	-----	-----

Figure 13 - Continued 10

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1a	1a	1480
HCV-1	HCH-H	AAACCTTGGGGTATGTGCCGCCAGAGTGTC
HC-J1	HC-V-J	-G-----T-C-----A-----C-----
HCV-BK	HCV-J4.83	-G-----T-C-----A-----C-----
HC-J4.91	HCV-JTA	CG-----G-----C-----T-----TC-CAG-----
HCV-JTB	HCV-CHINA	CC-----AA-----TACCC-----A-----T-----TC-GAG-----
HCV-T	HCV-JKL	CG-----G-----T-----C-----A-----T-----TC-GAG-----
HCUNK	1b	CG-----AG-----T-----C-----A-----T-----TC-CAG-----
HCV-N	1b	CG-----AG-----T-----C-----A-----T-----TC-CAG-----
HC-J6	2a	CG-----AG-----T-----C-----A-----T-----TC-CAG-----
HC-J8	2b	CG-----G-----T-----C-----A-----T-----TC-CAG-----
HC-J5	2a	CG-----G-----T-----C-----A-----T-----TC-CAG-----
HC-J7	3a	CG-----G-----T-----C-----A-----T-----TC-CAG-----
NZL1	3a	CG-----TACCG-----C-----A-----ATCA-----C-----
HEM26	3a	CG-----TAAA-----G-----C-----A-----ATCA-----C-----
TH85	3a	CG-----T-----A-----CC-----C-----G-----ATCA-----C-----
US114	5a	CG-----G-----AG-G-----A-----CC-----AGAG-----C-----
BE95		

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COPY

RULE 63 (37 C.F.R. 1.63)
DECLARATION AND POWER OF ATTORNEY
FOR PATENT APPLICATION
IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

As a below-named inventor, I hereby declare that my residence, post office address and citizenship are as stated below next to my name, and I believe I am the original first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled: "NEW SEQUENCES OF HEPATITIS C US GENOTYPES AND THEIR USE AS THERAPEUTIC AND DIAGNOSTIC AGENTS"

the specification or which (check applicable box(s))

is attached hereto
 was filed on _____ as U.S. Application Serial No. _____ (Atty Dkt. No. _____)
 was filed as PCT International application No. PCT EP94/01323 on 27 APRIL 1994
 and (if applicable to U.S. or PCT application) was amended on _____

I hereby state that I have reviewed and understand the contents of the above-mentioned specification, including the claims, as amended by any amendment referred to above. I acknowledge the duty to disclose information which is material to the patentability of this application in accordance with 37 C.F.R. 1.56. I hereby claim foreign priority benefits under 35 U.S.C. 119/365 of any foreign application(s) for patent or inventor's certificate listed below and have also identified below any foreign application for patent or inventor's certificate having a filing date before that of the application on which priority is claimed or, if no priority is claimed, before the filing date of this application.

Prior Foreign Application(s):

Application Number	Country	Day/Month/Year Filed
93.401 099.2	EUROPE	27 APRIL 1993
93.402.019.9	EUROPE	05 AUGUST 1993

I hereby claim the benefit under 35 U.S.C. 120/365 of all prior United States and PCT International applications listed above or below and, insofar as the subject matter of each of the claims of this application is not disclosed in such prior applications in the manner provided by the first paragraph of 35 U.S.C. 112, I acknowledge the duty to disclose material information as defined in 37 C.F.R. 1.56 which occurred between the filing date of the prior applications and the national or PCT International filing date of this application.

Prior U.S./PCT Application(s):
 Application Serial No. Day/Month/Year Filed Status: patented, pending, abandoned

PCT/EP94/01323	27 APRIL 1994	PENDING
----------------	---------------	---------

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true, and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 101 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issued thereon. And I hereby appoint NIXON & VANDERHUYSE P.C. 1100 North Glebe Rd., 3rd Floor, Arlington, VA 22201-4714, telephone number (703) 316-4000 (to whom all communications are to be directed), and the following attorneys thereof (at the same address) individually and collectively my attorneys to prosecute this application and to transact all business in the Patent and Trademark Office connected therewith and with the resulting patent: Arthur R. Crawford, 25327; Larry S. Nixon, 25640; Robert A. Vandervive, 27076; James T. Hosmer, 30184; Robert W. Fans, 31352; Richard G. Besha, 22770; Mark E. Neubaum, 32248; Michael J. Keenan, 32106; Bryan H. Davidson, 30251; Stanley C. Scooner 27393; Leonard C. Mitchell, 29009; Duane M. Evers, 33362; Paul J. Henon, 33626; Jeffry H. Nelson, 30481; John R. Lastova, 33149; H. Warren Burman, Jr., 29366; Thomas E. Byrne, 32205; Mary J. Wilson, 32955; J. Scott Davidson, 33489.

1. Inventor's Signature:

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(Zip Code): <u>B-8310 BRUGGE</u>	<u>BELGIUM</u>		

2. Inventor's Signature:

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Residence (city): <u>B-9340 LEDE</u>	(state/country): <u>BELGIUM</u>	(citizenship)	
Post Office Address: <u>Hoogstraat 27</u>			
(Zip Code): <u>B-9340 LEDE</u>	<u>BELGIUM</u>		

3. Inventor's Signature:

Inventor:	(first)	(last)	Date
Residence (city):		(state/country):	
Post Office Address:			
(Zip Code):			

FOR ADDITIONAL INVENTORS, check box and attach sheet with same information and signature and date for each.

WO 94/25601

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: Innogenetics sa.
- (B) STREET: Industriepark Zwijnaarde 7, box 4
- (C) CITY: Ghent
- (E) COUNTRY: Belgium
- (F) POSTAL CODE (ZIP): B-9052
- (G) TELEPHONE: 00 32 9 241 07 11
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(ii) TITLE OF INVENTION: New sequences of hepatitis C virus genotypes
for diagnosis, prophylaxis and therapy.

(iii) NUMBER OF SEQUENCES: 270

(iv) COMPUTER READABLE FORM.

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: BR34-4-20

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..213

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CTC ACG GAA CGG CTT TAC TGC GGG GGC CCT ATG TTC AAC AGC AAG GGG
 Leu Thr Glu Arg Leu Tyr Cys Gly-Gly Pro Met Phe Asn Ser Lys Gly
 1 5 10 15

48

GCC CAG TGT GGT TAT CGC CGC TGC CGT GCC AGT GGA GTT CTG CCT ACC
 Ala Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr

96

20	96	30	
AGC TTC GGC AAC ACA ATC ACT TGC TAC ATC AAG GCC ACA GCG GCT GCA Ser Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Ala Ala Ala			144
35	40	45	
AGG GCC GCA GGC CTC CGG AAC CCG GAC TTT CTT GTC TGC GGA GAT GAT Arg Ala Ala Gly Leu Arg Asn Pro Asp Phe Leu Val Cys Gly Asp Asp			192
50	55	60	
CTG GTC GTG GTG GCT GAG AGT Leu Val Val Val Ala Glu Ser			213
65	70		

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Leu Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly			
1	5	10	15
Ala Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr			
20	25	30	
Ser Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Ala Ala Ala			
35	40	45	
Arg Ala Ala Gly Leu Arg Asn Pro Asp Phe Leu Val Cys Gly Asp Asp			
50	55	60	
Leu Val Val Val Ala Glu Ser			
65	70		

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (B) CLONE: BR36-23-18

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..213

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

CTC ACG GAA CGG CTT TAC TGC GGG GGC CCT ATG TTC AAC AGC AAG GGG	48
Leu Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly	
1 5 10 15	
GCC CAG TGT GGT TAT CGC CGC TGC CGT GCC AGT GGA GTT CTG CCT ACC	96
Ala Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr	
20 25 30	
AGC TTC GGC AAC ACA ATC ACT TGC TAC ATC AAG GCC ACA GCG GCT GCA	144
Ser Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Ala Ala Ala	
35 40 45	
AGG GCC GCA GGC CTC CGG AAC CCG GAC TTT CTT GTC TGC GGA GAT GAT	192
Arg Ala Ala Gly Leu Arg Asn Pro Asp Phe Leu Val Cys Gly Asp Asp	
50 55 60	
CTG GTC GTG GTG GCT GAG AGT	213
Leu Val Val Val Ala Glu Ser	
65 70	

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Leu Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly	
1 5 10 15	
Ala Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr	
20 25 30	
Ser Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Ala Ala Ala	
35 40 45	
Arg Ala Ala Gly Leu Arg Asn Pro Asp Phe Leu Val Cys Gly Asp Asp	
50 55 60	
Leu Val Val Val Ala Glu Ser	
65 70	

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(iii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: BR36-23-18

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..213

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CTC ACG GAG CGG CTT TAC TGC GGG GGC CCT ATG TTT AAC AGC AAG GGG	48
Leu Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly	
1 5 10 15	
GCC CAG TGT GGT TAT CGC CGT TGC CGT GCC AGT GGA GTT CTG CCT ACC	96
Ala Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr	
20 25 30	
AGC TTC GGC AAC ACA ATC ACT TGT TAC ATC AAA GCC ACA GCG GCC GCA	144
Ser Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Ala Ala Ala	
35 40 45	
AAA GCC GCA GGC CTC CGG AGC CGG GAC TTT CTT GTC TGC GGA GAT GAT	192
Lys Ala Ala Gly Leu Arg Ser Pro Asp Phe Leu Val Cys Gly Asp Asp	
50 55 60	
CTG GTC GTG GTG GCT GAG AGT	
Leu Val Val Val Ala Glu Ser	
65 70	

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Leu Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly	
1 5 10 15	
Ala Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr	
20 25 30	
Ser Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Ala Ala Ala	
35 40 45	

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Lys	Ala	Ala	Gly	Leu	Arg	Ser	Pro	Asp	Phe	Leu	Val	Cys	Gly	Asp	Asp
50				55						60					

Leu	Val	Val	Val	Ala	Glu	Ser
65				70		

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: BR36-23-20

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..213

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

CTC ACG GAG CGG CTT TAC TGC GGG GGC CCT ATG TTT AAC AGC AAA GGG	48		
Leu Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly			
1	5	10	15
GCC CAG TGT GGT TAT CGC CGT TGC CGT GCC AGT GGA GTT CTG CCT ACC	95		
Ala Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr			
20	25	30	
AGC TTC GGC AAC ACA ATC ACT TGT TAC ATC AAA GCC ACA GCG GCC GCA	144		
Ser Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Ala Ala Ala			
35	40	45	
AAA GCC GCA GGC CTC CGG AGC CCG GAC TTT CTT GTC TGC GGA GAT GAT	192		
Lys Ala Ala Gly Leu Arg Ser Pro Asp Phe Leu Val Cys Gly Asp Asp			
50	55	60	
CTG GTC GTG GTG GCT GAG AGT	213		
Leu Val Val Val Ala Glu Ser			
65	70		

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Leu Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly
 1 5 10 15

Ala Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr
 20 25 30

Ser Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Ala Ala Ala
 35 40 45

Lys Ala Ala Gly Leu Arg Ser Pro Asp Phe Leu Val Cys Gly Asp Asp
 50 55 60

Leu Val Val Val Ala Glu Ser
 65 70

(2) INFORMATION FOR SEQ ID NO: 9.

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: BR33-2-17

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..213

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

CTC ACG GAG CGG CTT TAC TGC GGG GGC CCT ATG TTC AAC AGC AAG GGG	48
Leu Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly	
1 5 10 15	
GCC CAG TGT GGT TAT CGC CGT TGT CGT GCC AGT GGA GTT CTG CCT ACC	96
Ala Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr	
20 25 30	
AGT TTC GGC AAC ACA ATC ACT TGT TAC ATC AAG GCC ACA GCG GCT GCA	144
Ser Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Ala Ala Ala	
35 40 45	
AAA GCC GCA GGC CTC CGG AAC CCG GAC TTT CTT GTT TGC GGA GAT GAT	192

101
Lys Ala Ala Gly Leu Arg Asn Pro Asp Phe Leu Val Cys Gly Asp Asp
50 55 60

TTG GTC GTG GTG GCT GAG AGT 213
Leu Val Val Val Ala Glu Ser
65 70

(2) INFORMATION FOR SEQ ID NO: 10:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 71 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Leu Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly
1 5 10 15

Ala Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr
20 25 30

Ser Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Ala Ala Ala
35 40 45

Lys Ala Ala Gly Leu Arg Asn Pro Asp Phe Leu Val Cys Gly Asp Asp
50 55 60

Leu Val Val Val Ala Glu Ser
65 70

(2) INFORMATION FOR SEQ ID NO: 11:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 213 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
(B) CLONE: BR33-2-21

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..213

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

CTC ACG GAG CGG CTT TAC TGC GGG GGC CCT ATG TTC AAC AGC AAG GGG Leu Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly	48
1 5 10 15	
GCC CAG TGT GGT TAT CGC CGT TGT CGT GCC AGT GGA GTT CTG CCT ACC Ala Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr	96
20 25 30	
AGT TTC GGC AAC ACA ATC ACT TGT TAC ATC AAG GGC ACA GCG GCT GCA Ser Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Ala Ala Ala	144
35 40 45	
AAA GCC GCA GGC CTC CGG AAC CCG GAC TTT CTT GTT TGC GGA GAT GAT Lys Ala Ala Gly Leu Arg Asn Pro Asp Phe Leu Val Cys Gly Asp Asp	192
50 55 60	
TTG GTC GTG GTG GCT GAG AGT Leu Val Val Val Ala Glu Ser	213
65 70	

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Leu Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly 1 5 10 15	
Ala Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr 20 25 30	
Ser Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Ala Ala Ala 35 40 45	
Lys Ala Ala Gly Leu Arg Asn Pro Asp Phe Leu Val Cys Gly Asp Asp 50 55 60	
Leu Val Val Val Ala Glu Ser 65 70	

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 541 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE:

(B) CLONE: HD10-2-5

(ix) FEATURE:

(A) NAME / KEY : CD

(B) LOCATION: 2..541

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

C GTC GGC GCT CCT GTA GGA GGC GTC GCA AGA GCC CTT GCG CAT GGC Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly	1	5	10	15	46
GTG AGG GCC CTT GAA GAC GGG ATA AAT TTC GCA ACA GGG AAT TTG CCC Val Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro	20	25	30		94
GGT TGC TCC TTT TCT ATC TTC CTT GCT CTG TTC TCT TGC TTA ATC Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile	35	40	45		142
CAT CCA GCA GCT AGT CTA GAG TGG CGG AAC ACG TCT GGC CTC TAT GTC His Pro Ala Ala Ser Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val	50	55	60		190
CTT ACC AAC GAC TGT TCC AAT AGC AGT ATT GTG TAT GAG GGC GAT GAC Leu Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp	65	70	75		238
GTT ATT CTG CAC ACA CCC GGC TGT GTA CCT TGT GTT CAG GAC GGT AAT Val Ile Leu His Thr Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn	80	85	90	95	286
ACA TCT GCG TGC TGG ACC CCA GTG ACA CCT ACA GTG GCA GTC AGG TAC Thr Ser Ala Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr	100	105	110		334
GTC GGA GCA ACC ACC GCT TCG ATA CGC AGG CAT GTA GAC ATG TTG GTG Val Gly Ala Thr Thr Ala Ser Ile Arg Arg His Val Asp Met Leu Val	115	120	125		382
GGC GCG GCC ACG ATG TGC TCT GCT CTC TAC GTG GGT GAT ATG TGT GGG Gly Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly	130	135	140		430
GCC GTC TTC CTC GTG GGA CAA GCC TTC ACG TTC AGA CCT CGT CGC CAT Ala Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His	145	150	155		478
CAA ACG GTC CAG ACC TGT AAC TGC TCA CTG TAC CCA GGC CAT CTT TCA Gln Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser	160	165	170	175	526

GGA CAC CGA ATG GCT
 Gly His Arg Met Ala
 180

541

(2) INFORMATION FOR SEQ ID NO: 14:

- (i) SEQUENCE CHARACTERISTICS.
- (A) LENGTH: 180 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Val	Gly	Ala	Pro	Val	Gly	Gly	Val	Ala	Arg	Ala	Leu	Ala	His	Gly	Val
1				5				10					15		
Arg	Ala	Leu	Glu	Asp	Gly	Ile	Asn	Phe	Ala	Thr	Gly	Asn	Leu	Pro	Gly
						20		25				30			
Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu	Phe	Ser	Cys	Leu	Ile	His
						35		40			45				
Pro	Ala	Ala	Ser	Leu	Glu	Trp	Arg	Asn	Thr	Ser	Gly	Leu	Tyr	Val	Leu
						50		55			60				
Thr	Asn	Asp	Cys	Ser	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	Asp	Asp	Val
						65		70			75		80		
Ile	Leu	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	Val	Gln	Asp	Gly	Asn	Thr
						85		90			95				
Ser	Ala	Cys	Trp	Thr	Pro	Val	Thr	Pro	Thr	Val	Ala	Val	Arg	Tyr	Val
						100		105			110				
Gly	Ala	Thr	Thr	Ala	Ser	Ile	Arg	Arg	His	Val	Asp	Met	Leu	Val	Gly
						115		120			125				
Ala	Ala	Thr	Met	Cys	Ser	Ala	Leu	Tyr	Val	Gly	Asp	Met	Cys	Gly	Ala
						130		135			140				
Val	Phe	Leu	Val	Gly	Gln	Ala	Phe	Thr	Phe	Arg	Pro	Arg	Arg	His	Gln
						145		150			155		160		
Thr	Val	Gln	Thr	Cys	Asn	Cys	Ser	Leu	Tyr	Pro	Gly	His	Leu	Ser	Gly
						165		170			175				
His	Arg	Met	Ala												
			180												

(2) INFORMATION FOR SEQ ID NO: 15:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 541 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: HD10-3-14

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 2..541

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

C GTC GGC GCT CCT GTA GGA GGC GTC GCA AGA GCC CTT GCG CAT GGC	1	5	10	15	46
Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly					
20	25	30			94
GTG AGG GCC CTT GAA GAC GGG ATA AAT TTC GCA ACA GGG AAT TTG CCC					
Val Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro					
35	40	45			142
GGT TGC TCC TTT TCT ATC TTC CTT CCT GCT CTG TTC TCT TGC TTA ATC					
Gly Cys Ser Phe Ser Ile Phe Leu Pro Ala Leu Phe Ser Cys Leu Ile					
50	55	60			190
CAT CCA GCA GCT AGT CTA GAG TGG CGG AAC ACG TCT GGC CTC TAT GTC					
His Pro Ala Ala Ser Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val					
65	70	75			238
CTT ACC AAC GAC TGT TCC AAT AGC AGT ATT GTG TAT GAG GCC GAT GAC					
Leu Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp					
80	85	90	95		286
ACA TCT GCG TGC TGG ACC CCA GTG ACA CCT ACA GTG GCA GTC AGG TAC					
Thr Ser Ala Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr					
100	105	110			334
GTT ATT CTG CAC ACA CCC GGC TGT GTA CCT TGT GTT CAG GAC GGT AAT					
Val Ile Leu His Thr Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn					
115	120	125			382
GTC GGA GCA ACC ACC GCT TCG ATA CGC AGG CAT GTA GAC ATA TTG GTG					
Val Gly Ala Thr Thr Ala Ser Ile Arg Arg His Val Asp Ile Leu Val					
130	135	140			430
GCC GTC TTC CTC GTG GGA CAA GCC TTC ACG TTC AGA CCT CGT CGC CAT					
Ala Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His					
145	150	155			478
CAA ACG GTC CAG ACC TGT AAC TGC TCA CTG TAC CCA GGC CAT CTT TCA					526

Gln Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser
 160 165 170 175

GGA CAC CGA ATG GCT 541
Gly His Arg Met Ala
180

(2) INFORMATION FOR SEQ ID NO: 16:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 190 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val
1 5 10 15

Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro Gly
20 25 30

Cys Ser Phe Ser Ile Phe Leu Pro Ala Leu Phe Ser Cys Leu Ile His
35 40 45

Pro Ala Ala Ser Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val Leu
50 55 60

Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Val
65 70 75 80

Ile Leu His Thr Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn Thr
85 90 95

Ser Ala Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr Val
100 105 110

Gly Ala Thr Thr Ala Ser Ile Arg Arg His Val Asp Ile Leu Val Gly
115 120 125

Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly Ala
 130 135 140

Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His Gln
145 150 155 160

Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser Gly
165 170 175

His Arg Met Ala
190 -

(2) INFORMATION

100-100

(2) INFORMATION FOR SEQ ID NO: 17 :

- (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 541 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: HD10-2-21

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..541

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

C GTC GGC GCT CCT GTA GGA GGC GTC GCA AGA GCC CTT GCG CAT GGC	46
Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly	
1 5 10 15	
GTG AGG GCC CTT GAA GAC GGG ATA AAT TTC GCA ACA GGG AAT TTG CCC	94
Val Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro	
20 25 30	
GGT TGC TCC TTT TCT ATC TTC CTT GCT CTG TTC TCT TGC TTA ATC	142
Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile	
35 40 45	
CAT CCA GCA GCT AGT CTA GAG TGG CGG AAC ACG TCT GGC CTC TAC GTC	190
His Pro Ala Ala Ser Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val	
50 55 60	
CTT ACC AAC GAC TGT TCC AAT AGC AGT ATT GTG TAT GAG GCC GAT GAC	238
Leu Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp	
65 70 75	
GTT ATT CTG CAC ACA CCC GGC TGT GTA CCT TGT GTT CAG GAC GGT AAT	286
Val Ile Leu His Thr Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn	
80 85 90 95	
ACA TCT GCG TGC TGG ACC CCA GTG ACA CCT ACA GTG GCA GTC AGG TAC	334
Thr Ser Ala Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr	
100 105 110	
GTC GGA GCA ACC ACC GCT TCG ATA CGC AGG CAT GTA GAC ATA TTG GTG	382
Val Gly Ala Thr Thr Ala Ser Ile Arg Arg His Val Asp Ile Leu Val	
115 120 125	
GGC GCG GCC ACG ATG TGC TCT GCT CTC TAC GTG GGT GAT ATG TGT GGG	430
Gly Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly	
130 135 140	

GCC GTC TTC CTC GTG GGA CAA GCC TTC ACG TTC AGA CCT CGT CGC CAT Ala Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His 145 150 155	478
CAA ACG GTC CAG ACC TGT AAC TGC TCA CTG TAC CCA GGC CAT CTT TCA Gln Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser 160 165 170 175	526
GGA CAC CGA ATG GCT Gly His Arg Met Ala 180	541

(2) INFORMATION FOR SEQ ID NO: 18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 180 amino acids
 - (B) TYPE: amino acid
 - (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18.

Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val 1 5 10 15
Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro Gly 20 25 30
Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile His 35 40 45
Pro Ala Ala Ser Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val Leu 50 55 60
Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Val 65 70 75 80
Ile Leu His Thr Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn Thr 85 90 95
Ser Ala Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr Val 100 105 110
Gly Ala Thr Thr Ala Ser Ile Arg Arg His Val Asp Ile Leu Val Gly 115 120 125
Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly Ala 130 135 140
Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His Gln 145 150 155 160
Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser Gly 165 170 175
His Arg Met Ala

180

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 541 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: BR36-9-13

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..541

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

C GTC GGC GCT CCC GTA GGA GGC GTC GCA AGA GCC CTT GCG CAT GGC	46
Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly	
1 S 10 15	
GTG AGG GCC CTT GAA GAC GGG ATA AAT TTC GCA ACA GGG AAT TTG CCC	94
Val Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro	
20 25 30	
GGT TGC TCC TTT TCT ATT TTC CTT GCT CTG TTC TCT TGC TTA ATT	142
Gly Cys Ser Phe Ser Ile Phe Leu Ala Leu Phe Ser Cys Leu Ile	
35 40 45	
CAT CCA GCA GCT AGT CTA GAG TGG CGG AAT ACG TCT GGC CTC TAT GTC	190
His Pro Ala Ala Ser Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val	
50 55 60	
CTT ACC AAC GAC TGT TCC AAT AGC AGT ATT GTG TAC GAG GCC GAT GAC	238
Leu Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp	
65 70 75	
GTT ATT CTG CAC ACA CCC GGC TGC ATA CCT TGT GTC CAG GAC GGC AAT	286
Val Ile Leu His Thr Pro Gly Cys Ile Pro Cys Val Gln Asp Gly Asn	
80 85 90 95	
ACA TCC ACG TGC TGG ACC CCA GTG ACA CCT ACA GTG GCA GTC AAG TAC	334
Thr Ser Thr Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Lys Tyr	
100 105 110	
GTC GGA GCA ACC ACC GCT TCG ATA CGC AGT CAT GTG GAC CTA TTA GTG	382
Val Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val	
115 120 125	

GCG GCG GCC ACG ATG TGC TCA GCG CTC TAC GTG GGT GAT ATG TGT GGG	430		
Gly Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly			
130	135	140	
GCC GTC TTC CTT GTG GGA CAA GCC TTC ACG TTC AGA CCT CGT CGC CAT	478		
Ala Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His			
145	150	155	
CAG ACG GTC CAG ACC TGT AAC TGC TCG CTG TAC CCA GGC CAT CTT TCA	526		
Gin Thr Val Gin Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser			
160	165	170	175
GGA CAT CGA ATG GCT	541		
Gly His Arg Met Ala			
180			

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

Val Gly Ala Pro Val Gly Val Ala Arg Ala Leu Ala His Gly Val			
1	5	10	15
Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro Gly			
20	25	30	
Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile His			
35	40	45	
Pro Ala Ala Ser Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val Leu			
50	55	60	
Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Val			
65	70	75	80
Ile Leu His Thr Pro Gly Cys Ile Pro Cys Val Gln Asp Gly Asn Thr			
85	90	95	
Ser Thr Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Lys Tyr Val			
100	105	110	
Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val Gly			
115	120	125	
Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly Ala			
130	135	140	
Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His Gln			
145	150	155	160
Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser Gly			

165

170

175

His Arg Met Ala
180

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 541 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: BR36-9-20

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..541

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

C GTC GGC GCT CCC GTA GGA GGC GTC GCA AGA GCC CTT GCG CAT GGC	46
Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly	
1 5 10 15	
GTG AGG GCC CTT GAA GAC GGG ATA AAT TTC GCA ACA GGG AAT TTG CCC	94
Val Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro	
20 25 30	
GGT TGC TCC TTT TCT ATT TTC CTT CTT GCT CTG TTC TTT TGC TTA ATT	142
Gly Cys Ser Phe Ser Ile Phe Leu Ala Leu Phe Ser Cys Leu Ile	
35 40 45	
CAT CCA GCA GCT AGT CTA GAG TGG CGG AAT ACG TCT GGC CTC TAT GTC	190
His Pro Ala Ala Ser Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val	
50 55 60	
CTT ACC AAC GAC TGT TCC AAT AGC AGT ATT GTG TAC GAG GCC GAT GAC	238
Leu Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp	
65 70 75	
GTG ATT CTG CAC ACA CCC GGC TGC ATA CCT TGT GTC CAG GAC GGC AAT	286
Val Ile Leu His Thr Pro Gly Cys Ile Pro Cys Val Gln Asp Gly Asn	
80 85 90 95	
ACA TCC ACG TGC TGG ACC CCA GTG ACA CCT ACA GTG GCA GTC AAG TAC	334
Thr Ser Thr Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Lys Tyr	
100 105 110	

GTC GGA GCA ACC ACC GCT TCG ATA CGC AGT CAT GTG GAC CTA TTA GTG	382
Val Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val	
115 120 125	
 GGC GCG GCC ACG ATG TGC TCT GCG CTC TAC GTG GGT GAC ATG TGT GGG	430
Gly Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly	
130 135 140	
 GCT GTC TTC CTC GTG GGA CAA GCC TTC ACG TTC AGA CCT CGT CGC CAT	478
Ala Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His	
145 150 155	
 CAA ACG GTC CAG ACC TGT AAC TGC TCG CTG TAC CCA GGC CAT CTT TCA	526
Gln Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser	
160 165 170 175	
 GGA CAT CGA ATG GCT	541
Gly His Arg Met Ala	
180	

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val	
1 5 10 15	
 Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro Gly	
20 25 30	
 Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile His	
35 40 45	
 Pro Ala Ala Ser Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val Leu	
50 55 60	
 Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Val	
65 70 75 80	
 Ile Leu His Thr Pro Gly Cys Ile Pro Cys Val Gln Asp Gly Asn Thr	
85 90 95	
Ser Thr Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Lys Tyr Val	
100 105 110	
 Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val Gly	
115 120 125	
 Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly Ala	
130 135 140	

Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His Gln
145 150 155 160

Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser Gly
165 170 175

His Arg Met Ala
180

(2) INFORMATION FOR SEQ ID NO: 23:

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 541 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NC

(1ii) ANTI-SENSE: NC

(vi) IMMEDIATE SOURCE.

(S) CLONE: BR33-1-10

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 2..541

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

C GTC GGC GCT CCC GTA GGA GGC GTC GCA AGA GCC CTT GCG CAT GGC	45
Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly	
1 5 10 15	
 GTG AGG GCC CTT GAG GAC GGG ATA AAC TTC GCA ACA GGG AAT TTG CCC	94
Val Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro	
20 25 30	
 GGT TGC TCC TTT TCT ATC TTC CTT CTT GCT CTG TTC TCT TGC TTA ATC	142
Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile	
35 40 45	
 CAT CCA GCA GCT GGT CTA GAG TGG CGG AAT ACG TCT GGC CTC TAT GTC	190
His Pro Ala Ala Gly Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val	
50 55 60	
 CTT ACC AAC GAC TGT TCC AAT AGT AGT ATT GTG TAT GAG GCC GAT GAC	238
Leu Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp	
65 70 75	
 GTT ATT CTG CAC GCG CCC GGC TGT GTA CCT TGT GTC CAG GAC GGC AAT	283
Val Ile Leu His Ala Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn	
80 85 90 95	

ACG TCT ACA TGC TGG ACC CCA GTA ACA CCT ACA GTG GCA GTC AGG TAC	334
Thr Ser Thr Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr	
100	105
110	
GTC GGG GCA ACI ACC GCT TCG ATA CGC AGT CAT GTG GAC CTG TTA GTA	382
Val Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val	
115	120
125	
GCC GCG GCC ACG ATG TGC TCT GCG CTT TAC GTG GGT GAT ATG TGT GGG	430
Gly Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly	
130	135
140	
GCC GTC TTC CTC GTG GGA CAA GCC TTC ACG TTC AGA CCC CGC CGC CAT	478
Ala Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His	
145	150
155	
CAA ACG GTC CAG ACC TGT AAC TGC TCG CTG TAC CCA GGC CAT CTT TCA	526
Gln Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser	
160	165
170	175
GGA CAT CGC ATG GCT	541
Gly His Arg Met Ala	
180	

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 180 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val			
1	5	10	15
Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro Gly			
20	25	30	
Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile His			
35	40	45	
Pro Ala Ala Gly Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val Leu			
50	55	60	
Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Val			
65	70	75	80
Ile Leu His Ala Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn Thr			
85	90	95	
Ser Thr Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr Val			
100	105	110	
Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val Gly			

115 120 125

Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly Ala
 130 135 140

Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His Gln
 145 150 155 160

Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser Gly
 165 170 175

His Arg Met Ala
 180

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 541 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: BR33-1-19

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..541

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

C GTC GGC GCT CCC GTA GGA GGC GTC GCA AGA GCC CTT GCG CAT GGC	46
Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly	
1 5 10 15	
GTG AGG GCC CTT GAG GAC GGG ATA AAC TTC GCA ACA GGG AAT TTG CCC	94
Val Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro	
20 25 30	
GGT TGC TCT TTT TCT ATC TTC CTT GCT CTG TTC TCT TGC TTA ATC	142
Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile	
35 40 45	
CAT CCA GCA GCT GGT CTA GAG TGG CGG AAT ACG TCT GGC CTC TAT GTC	190
His Pro Ala Ala Gly Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val	
50 55 60	
CTT ACC AAC GAC TGT TCC AAT AGT AGT ATT GTG TAT GAG GCC GAT GAC	238
Leu Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp	
65 70 75	

GTT ATT CTG CAC GCG CCC GGC TGT GTA CCT TGT GTC CAG GAC GGC AAT Val Ile Leu His Ala Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn 80 85 90 95	286
ACG TCT ACA TGC TGG ACC CCA GTA ACA CCT ACA GTG GCA GTC AGG TAC Thr Ser Thr Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr 100 105 110	334
GTC GGG GCA ACC ACC GCT TCG ATA CGC AGT CAT GTG GAC CTG TTA GTA Val Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val 115 120 125	382
GGC GCG GCC ACG ATG TGC TCT GCG CTT TAC GTG GGT GAT ATG TGT GGG Gly Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly 130 135 140	430
GCC GTC TTC CTC GTG GGA CAA GCC TTC ACG TTC AGA CCC CGC CGC CAT Ala Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His 145 150 155	478
CAA ACG GTC CAG ACC TGT AAC TGC TCG CTG TAC CCA GGC CAT CTT TCA Gln Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser 160 165 170 175	526
GGA CAT CGA ATG GCT Gly His Arg Met Ala 180	541

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val 1 5 10 15
Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro Gly 20 25 30
Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile His 35 40 45
Pro Ala Ala Gly Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val Leu 50 55 60
Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Val 65 70 75 80
Ile Leu His Ala Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn Thr 85 90 95

Ser Thr Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr Val
 100 105 110

Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val Gly
 115 120 125

Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly Ala
 130 135 140

Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His Gln
 145 150 155 160

Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser Gly
 165 170 175

His Arg Met Ala
 180

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 541 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: BR33-1-20

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..541

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

C GTC GGC GCT CCC GTA GGA GGC GTC GCA AGA GCC CTT GCG CAT GGC	46
Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly	
1 5 10 15	
GTG AGG GCC CTT GAG GAC GGG ATA AAC TTC GCA ACA GGG AAT TTG CCC	94
Val Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro	
20 25 30	
GGT TGC TCT TTT TCT ATC TTC CTT GCT CTG TTC TCT TGC TTA ATC	142
Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile	
35 40 45	
CAT CCA GCA GCT GGT CTA GAG TGG CGG AAT ACG TCT GGC CTC TAT GTC	190
His Pro Ala Ala Gly Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val	
50 55 60	

CTT ACC AAC GAC TGT TCC AAT AGT AGT ATT GTG TAT GAG GCC GAT GAC Leu Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp	65	70	75	238
GTT ATT CTG CAC GCG CCC GGC TGT GTA CCT TGT GTC CAG GAC GGC AAT Val Ile Leu His Ala Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn	80	85	90	286
ACG TCT ACA TGC TGG ACC CCA GTA ACA CCT ACA GTG GCA GTC AGG TAC Thr Ser Thr Cys Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr	100	105	110	334
GTC GGG GCA ACC ACC GCT TCG ATA CGC AGT CAT GTG GAC CTG TTA GTA Val Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val	115	120	125	382
GCG GCG GCC ACG ATG TGC TCT GCG CTT TAC GTG GGT GAT ATG TGT GGG Gly Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly	130	135	140	430
GCC GTC TTC CTC GTG GGA CAA GCC TTC ACG TTC AGA CCC CGC CGC CAT Ala Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His	145	150	155	478
CAA ACG GTC CAG ACC TGT AAC TGC TCG CTG TAC CCA GGC CAT CTT TCA Gln Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser	160	165	170	526
GGA CAT CGA ATG GCT Gly His Arg Met Ala	180			541

(2) INFORMATION FOR SEQ ID NO: 28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 180 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Val	Gly	Ala	Pro	Val	Gly	Gly	Val	Ala	Arg	Ala	Leu	Ala	His	Gly	Val
1				5				10					15		
Arg	Ala	Leu	Glu	Asp	Gly	Ile	Asn	Phe	Ala	Thr	Gly	Asn	Leu	Pro	Gly
				20				25					30		
Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu	Phe	Ser	Cys	Leu	Ile	His
						35		40				45			
Pro	Ala	Ala	Gly	Leu	Glu	Trp	Arg	Asn	Thr	Ser	Gly	Leu	Tyr	Val	Leu
						50		55				60			
Thr	Asn	Asp	Cys	Ser	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	Asp	Asp	Val
						65		70			75				80

Ile Leu His Ala Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn Thr
 85 90 95

Ser Thr Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr Val
 100 105 110

Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val Gly
 115 120 125

Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly Ala
 130 135 140

Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His Gln
 145 150 155 160

Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser Gly
 165 170 175

His Arg Met Ala
 180

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 287 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NC

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
 (B) CLONE: HCCL153

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 3..287

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

TA GAC TTT TGG GAG AGC GTC TTC ACT GGA CTA ACT CAC ATA GAT GCC	47
Asp Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His Ile Asp Ala	
1 5 10 15	
CAC TTT CTG TCA CAG ACT AAG CAG CAG GGA CTC AAC TTC TCG TTC CTG	95
His Phe Leu Ser Gln Thr Lys Gln Gln Gly Leu Asn Phe Ser Phe Leu	
20 25 30	
ACT GCC TAC CAA GCC ACT GTG TGC GCT CGC GCG CAG GCT CCT CCC CCA	143
Thr Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala Pro Pro Pro	
35 40 45	
AGT TGG GAC GAG ATG TGG AAG TGT CTC GTC CGG CTT AAG CCA ACA CTA	191

120

Ser Trp Asp Glu Met Trp Lys Cys Leu Val Arg Leu Lys Pro Thr Leu			
50	55	60	
CAT GGA CCT ACG CCT CTT CTA TAT CGG TTG GGG CCT GTC CAA AAT GAA			239
His Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Pro Val Gln Asn Glu			
65	70	75	
ATC TGC TTG ACR CAC CCC ATC ACA ARA TAC ATC ATG GCA TGC ATG TCA			287
Ile Cys Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met Ser			
80	85	90	95

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 95 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30.

Asp Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His Ile Asp Ala His			
1	5	10	15
Phe Leu Ser Gln Thr Lys Gln Gln Gly Leu Asn Phe Ser Phe Leu Thr			
20	25	30	
Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala Pro Pro Pro Ser			
35	40	45	
Trp Asp Glu Met Trp Lys Cys Leu Val Arg Leu Lys Pro Thr Leu His			
50	55	60	
Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Pro Val Gln Asn Glu Ile			
65	70	75	80
Cys Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met Ser			
85	90	95	

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS.
 (A) LENGTH: 401 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
 (B) CLONE: HD10-1-25

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 3..401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

TC CAA AAT GAA ATC TGC TTG ACA CAC CCC GTC ACA AAA TAC ATT ATG Gln Asn Glu Ile Cys Leu Thr His Pro Val Thr Lys Tyr Ile Met	47
1 5 10 15	
GCA TGC ATG TCA GCT GAT CTG GAA GTA ACC ACC AGC ACC TGG GTG TTG Ala Cys Met Ser Ala Asp Leu Glu Val Thr Thr Ser Thr Trp Val Leu	95
20 25 30	
CTT GGA GGG GTC CTC GCG GCC CTA GCG GCC TAC TGC TTG TCA GTC GGC Leu Gly Val Leu Ala Ala Leu Ala Tyr Cys Leu Ser Val Gly	143
35 40 45	
TGC GTT GTA ATC GTG GGT CRT ATC GAG CTG GGG GGC AAG CCG GCA CTC Cys Val Val Ile Val Gly His Ile Glu Leu Gly Gly Lys Pro Ala Leu	191
50 55 60	
GTT CCA GAC AAG GAG GTG TTG TAT CAA CAG TAC GAT GAG ATG GAG GAG Val Pro Asp Lys Glu Val Leu Tyr Gln Gln Tyr Asp Glu Met Glu Glu	239
65 70 75	
TGC TCG CAA GCC GCC CCA TAC ATC GAA CAA GCT CAG GTA ATA GCC CAC Cys Ser Gln Ala Ala Pro Tyr Ile Glu Gln Gln Val Ile Ala His	287
80 85 90 95	
CAG TTC AAG GAG AAA ATC CTT GGA CTG CTG CAG CGA GCC ACC CAA CAA Gln Phe Lys Glu Ile Leu Glu Leu Gln Arg Ala Thr Gln Gln	335
100 105 110	
CAA GCT GTC ATT GAG CCC GTC ATA GCT TCC AAC TGG CAA AAG CTT GAA Gln Ala Val Ile Glu Pro Val Ile Ala Ser Asn Trp Gln Lys Leu Glu	383
115 120 125	
ACC TTC TGG CAC AAG CAT Thr Phe Trp His Lys His	401
130	

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

Gln Asn Glu Ile Cys Leu Thr His Pro Val Thr Lys Tyr Ile Met Ala	
1 5 10 15	

Cys Met Ser Ala Asp Leu Glu Val Thr Thr Ser Thr Trp Val Leu Leu
 20 25 30

Gly Gly Val Leu Ala Ala Leu Ala Ala Tyr Cys Leu Ser Val Gly Cys
 35 40 45

Val Val Ile Val Gly His Ile Glu Leu Gly Lys Pro Ala Leu Val
 50 55 60

Pro Asp Lys Glu Val Leu Tyr Gln Gln Tyr Asp Glu Met Glu Glu Cys
 65 70 75 80

Ser Gln Ala Ala Pro Tyr Ile Glu Gln Ala Gln Val Ile Ala His Gln
 85 90 95

Phe Lys Glu Lys Ile Leu Gly Leu Leu Gln Arg Ala Thr Gln Gln Gln
 100 105 110

Ala Val Ile Glu Pro Val Ile Ala Ser Asn Trp Gln Lys Leu Glu Thr
 115 120 125

Phe Trp His Lys His
 130

(2) INFORMATION FOR SEQ ID NO: 33:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 401 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: HD10-1-3

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 3..401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

TC CAA AAT GAA ATC TGC TTG ACA CAC CCC GTC ACA AAA TAC ATT ATG	47
Gln Asn Glu Ile Cys Leu Thr His Pro Val Thr Lys Tyr Ile Met	
1 5 10 15	
GCA TGC ATG TCA GCT GAT CTG GAA GTA ACC ACC AGC ACC TGG GTG TTG	95
Ala Cys Met Ser Ala Asp Leu Glu Val Thr Thr Ser Thr Trp Val Leu	
20 25 30	
CTT GGA GGG GTC CTC GCG GCC CTA GCG GCC TAC TGC TTG TCA GTC GGC	143

WO 94/25601

123

Leu Gly Gly Val Leu Ala Ala Leu Ala Ala Tyr Cys Leu Ser Val Gly			
35	40	45	
TGC GTT GTA ATC GTG GGT CAT ATC GAG CTG GGG GGC AAG CCG GCA CTC		191	
Cys Val Val Ile Val Gly His Ile Glu Leu Gly Gly Lys Pro Ala Leu			
50	55	60	
GTT CCA GAC AAG GAG GTG TTG TAT CAA CGA TAC GAT GAG ATG GAG GAG		239	
Val Pro Asp Lys Glu Val Leu Tyr Gln Gln Tyr Asp Glu Met Glu Glu			
65	70	75	
TGC TCG CRA GCC GCC CCA TAC ATC GAA CAA GCT CAG GTA ATA GCC CAC		287	
Cys Ser Gln Ala Ala Pro Tyr Ile Glu Gln Ala Gln Val Ile Ala His			
80	85	90	95
CAG TTC AAG GAG AAA ATC CTT GGA CTG CTG CAG CGA GCC ACC CAA CAA		335	
Gln Phe Lys Glu Lys Ile Leu Gly Leu Leu Gln Arg Ala Thr Gln Gln			
100	105	110	
CAA GCT GTC ATT GAG CCC GTA ATA GCT TCC AAC TGG CAA AAG CTT GAA		383	
Gln Ala Val Ile Glu Pro Val Ile Ala Ser Asn Trp Gln Lys Leu Glu			
115	120	125	
ACC TTC TGG CAC AAG CAT		401	
Thr Phe Trp His Lys His			
130			

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

Gln Asn Glu Ile Cys Leu Thr His Pro Val Thr Lys Tyr Ile Met Ala			
1	5	10	15
Cys Met Ser Ala Asp Leu Glu Val Thr Thr Ser Thr Trp Val Leu Leu			
20	25	30	
Gly Gly Val Leu Ala Ala Leu Ala Ala Tyr Cys Leu Ser Val Gly Cys			
35	40	45	
Val Val Ile Val Gly His Ile Glu Leu Gly Gly Lys Pro Ala Leu Val			
50	55	60	
Pro Asp Lys Glu Val Leu Tyr Gln Gln Tyr Asp Glu Met Glu Glu Cys			
65	70	75	80
Ser Gln Ala Ala Pro Tyr Ile Glu Gln Ala Gln Val Ile Ala His Gln			
85	90	95	
Phe Lys Glu Lys Ile Leu Gly Leu Leu Gln Arg Ala Thr Gln Gln			

100

105

110

Ala Val Ile Glu Pro Val Ile Ala Ser Asn Trp Gln Lys Leu Glu Thr
 115 120 125

Phe Trp His Lys His
 130

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: BR36-20-164

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 3..401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

TC CAA AAT GAA ATC TGC TTG ACA CAC CCC ATC ACA AAA TAC ATC ATG
 Gln Asn Glu Ile Cys Leu Thr His Pro Ile Thr Lys Tyr Ile Met
 1 5 10 15

47

GCA TGC ATG TCA GCT GAT CTG GAA GTA ACC ACC AGC ACC TGG GTT TTG
 Ala Cys Met Ser Ala Asp Leu Glu Val Thr Thr Ser Thr Trp Val Leu
 20 25 30

95

CTT GGA GGG GTC CTC GCG GCC CTA GCG GCC TAC TGC TTG TCA GTC GGT
 Leu Gly Gly Val Leu Ala Ala Leu Ala Ala Tyr Cys Leu Ser Val Gly
 35 40 45

143

TGT GTT GTG ATT GTG GGT CAT ATC GAG CTG GGG GGC AAG CCG GCA ATC
 Cys Val Val Ile Val Gly His Ile Glu Leu Gly Gly Lys Pro Ala Ile
 50 55 60

191

GTT CCA GAC AAA GAG GTG TTG TAT CAA CAA TAC GAT GAG ATG GAA GAG
 Val Pro Asp Lys Glu Val Leu Tyr Gln Gln Tyr Asp Glu Met Glu Glu
 65 70 75

239

TGC TCA CAA GCT GCC CCA TAT ATC GAA CAA GCT CAG GTC ATA GCT CAC
 Cys Ser Gln Ala Ala Pro Tyr Ile Glu Gln Ala Gln Val Ile Ala His
 80 85 90 95

287

CAG TTC AAG GGA AAA GTC CTT GGA TTG CTG CAG CGA GCC ACC CAA CAA

335

125

Gln Phe Lys Gly Lys Val Leu Gly Leu Leu Gln Arg Ala Thr Gln Gln
 100 105 110

CAA GCT GTC ATT GAG CCC ATA GTA ACT ACC AAC TGG CAA AAG CTT GAG 383
 Gln Ala Val Ile Glu Pro Ile Val Thr Thr Asn Trp Gln Lys Leu Glu
 115 120 125

GCC TTT TGG CAC AAG CAT 401
 Ala Phe Trp His Lys His
 130

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

Gln Asn Glu Ile Cys Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala
 1 5 10 15

Cys Met Ser Ala Asp Leu Glu Val Thr Thr Ser Thr Trp Val Leu Leu
 20 25 30

Gly Gly Val Leu Ala Ala Leu Ala Ala Tyr Cys Leu Ser Val Gly Cys
 35 40 45

Val Val Ile Val Gly His Ile Glu Leu Gly Gly Lys Pro Ala Ile Val
 50 55 60

Pro Asp Lys Glu Val Leu Tyr Gln Gln Tyr Asp Glu Met Glu Glu Cys
 65 70 75 80

Ser Gln Ala Ala Pro Tyr Ile Glu Gln Ala Gln Val Ile Ala His Gln
 85 90 95

Phe Lys Gly Lys Val Leu Gly Leu Leu Gln Arg Ala Thr Gln Gln Gln
 100 105 110

Ala Val Ile Glu Pro Ile Val Thr Thr Asn Trp Gln Lys Leu Glu Ala
 115 120 125

Phe Trp His Lys His
 130

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: BR36-20-166

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 3..401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

TC CAA AAT GAA ATC TGC TTG ACA CAC CCC ATC ACA AAA TAC ATC ATG Gln Asn Glu Ile Cys Leu Thr His Pro Ile Thr Lys Tyr Ile Met 1 5 10 15	47
GCA TGC ATG TCA GCT GAT CTG GAA GTA ACC ACC AGC ACC TGG GTT TTG Ala Cys Met Ser Ala Asp Leu Glu Val Thr Thr Ser Thr Trp Val Leu 20 25 30	95
CTT GGA GGG GTC CTC GCG GCC CTA GCG GCC TAC TGC TTG TCA GTC GGT Leu Gly Gly Val Leu Ala Ala Leu Ala Ala Tyr Cys Leu Ser Val Gly 35 40 45	143
TGT GTT GTG ATT GTG GGT CAT ATC GAG CTG GGG GGC AAG CCG GCA ATC Cys Val Val Ile Val Gly His Ile Glu Leu Gly Gly Lys Pro Ala Ile 50 55 60	191
GTT CCA GAC AAA GAG GTG TTG TAT CAA CAA TAC GAT GAG ATG GAA GAG Val Pro Asp Lys Glu Val Leu Tyr Gln Gln Tyr Asp Glu Met Glu Glu 65 70 75	239
TGC TCA CAA GCT GCC CCA TAT ATC GAA CAA GCT CAG GTG ATA GCT CAC Cys Ser Gln Ala Ala Pro Tyr Ile Glu Gln Ala Gln Val Ile Ala His 80 85 90 95	287
CAG TTC AAG GAA AAA GTC CTT GGA TTG CTG CAG CGA GCC ACC CAA CAA Gln Phe Lys Glu Lys Val Leu Gly Leu Leu Gln Arg Ala Thr Gln Gln 100 105 110	335
CAA GCT GTC ATT GAG CCC ATA GTA ACT ACC AAC TGG CAA AAG CTT GAG Gln Ala Val Ile Glu Pro Ile Val Thr Thr Asn Trp Gln Lys Leu Glu 115 120 125	383
GCC TTT TGG CAC AAG CAT Ala Phe Trp His Lys His 130	401

(2) INFORMATION FOR SEQ ID NO: 38.

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 133 amino acids

- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

Gln Asn Glu Ile Cys Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala
1 5 10 15

Cys Met Ser Ala Asp Leu Glu Val Thr Thr Ser Thr Trp Val Leu Leu
20 25 30

Gly Gly Val Leu Ala Ala Leu Ala Ala Tyr Cys Leu Ser Val Gly Cys
35 40 45

Val Val Ile Val Gly His Ile Glu Leu Gly Gly Lys Pro Ala Ile Val
50 55 60

Pro Asp Lys Glu Val Leu Tyr Gln Gln Tyr Asp Glu Met Glu Glu Cys
65 70 75 80

Ser Gln Ala Ala Pro Tyr Ile Glu Gln Ala Gln Val Ile Ala His Gln
85 90 95

Phe Lys Glu Lys Val Leu Gly Leu Leu Gln Arg Ala Thr Gln Gln Gln
100 105 110

Ala Val Ile Glu Pro Ile Val Thr Thr Asn Trp Gln Lys Leu Glu Ala
115 120 125

Phe Trp His Lys His
130

(2) INFORMATION FOR SEQ ID NO: 39:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 401 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: BR36-20-165

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 3..401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

TC CAA AAT GAA ATC TGC TTG ACA CAC CCC ATC ACA AAA TAC ATC ATG Gln Asn Glu Ile Cys Leu Thr His Pro Ile Thr Lys Tyr Ile Met 1 5 10 15	47
GCA TGC ATG TCA GCT GAT CTG GAA GTA ACC ACC AGC ACC TGG GTT TTG Ala Cys Met Ser Ala Asp Leu Glu Val Thr Thr Ser Thr Trp Val Leu 20 25 30	95
CTT GGA GGG GTC CTC GCG GCC CTA GCG GCC TAC TGC TTG TCA GTC GGT Leu Gly Gly Val Leu Ala Ala Leu Ala Ala Tyr Cys Leu Ser Val Gly 35 40 45	143
TGT GTT GTG ATT GTG GGT CAT ATC GAG CTG GGG GGC AAG CCG GCA ATC Cys Val Val Ile Val Gly His Ile Glu Leu Gly Gly Lys Pro Ala Ile 50 55 60	191
GTT CCA GAC AAA GAG GTG TTG TAT CAA CAA TAC GAT GAG ATG GAA GAG Val Pro Asp Lys Glu Val Leu Tyr Gln Gln Tyr Asp Glu Met Glu Glu 65 70 75	239
TGC TCA CAA GCT GCC CCA TAT ATC GAA CAA GCT CAG GTC ATA GCT CAC Cys Ser Gln Ala Ala Pro Tyr Ile Glu Gln Ala Gln Val Ile Ala His 80 85 90 95	287
CAG TTC AAG GAA AAA GTC CTT GGA TTG CTG CAG CGA GCC ACC CAA CAA Gln Phe Lys Glu Lys Val Leu Gly Leu Leu Gln Arg Ala Thr Gln Gln 100 105 110	335
CAA GCT GTC ATT GAG CCC ATA GTC ACT ACC AAC TGG CAA AAG CTT GAG Gln Ala Val Ile Glu Pro Ile Val Thr Thr Asn Trp Gln Lys Leu Glu 115 120 125	383
GCC TTT TGG CAC AAG CAT Ala Phe Trp His Lys His 130	401

(2) INFORMATION FOR SEQ ID NO: 40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

Gln Asn Glu Ile Cys Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala 1 5 10 15
Cys Met Ser Ala Asp Leu Glu Val Thr Thr Ser Thr Trp Val Leu Leu 20 25 30
Gly Gly Val Leu Ala Ala Leu Ala Ala Tyr Cys Leu Ser Val Gly Cys 35 40 45

Val Val Ile Val Gly His Ile Glu Leu Gly Gly Lys Pro Ala Ile Val
 50 55 60

Pro Asp Lys Glu Val Leu Tyr Gln Gln Tyr Asp Glu Met Glu Glu Cys
 65 70 75 80

Ser Gln Ala Ala Pro Tyr Ile Glu Gln Ala Gln Val Ile Ala His Gln
 85 90 95

Phe Lys Glu Lys Val Leu Gly Leu Leu Gln Arg Ala Thr Gln Gln Gln
 100 105 110

Ala Val Ile Glu Pro Ile Val Thr Thr Asn Trp Gln Lys Leu Glu Ala
 115 120 125

Phe Trp His Lys His
 130

(2) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: PC-2-1

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 3..509

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

CC ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA AGA AAC ACC	47
Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr	
1 5 10 15	
AAC CGT CGC CCA CAG GAC GTC AAG TTC CCG GGC GGT GGT CAG ATC GTT	95
Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gln Ile Val	
20 25 30	
GGC GGA GTT TAC TTG TTG CCG CGC AGG GGC CCT AGG ATG GGT GTG CGC	143
Gly Gly Val Tyr Leu Leu Pro Arg-Arg Gly Pro Arg Met Gly Val Arg	
35 40 45	
GCG ACT CGG AAG ACT TCG GAA CGG TCG CAA CCC CGT GGA CGG CGT CAG	191
Ala Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln	

50	55	60	
CCT ATT CCC AAG GCG CGC CAG CCC ACG GGC CGG TCC TGG GGT CAA CCC Pro Ile Pro Lys Ala Arg Gln Pro Thr Gly Arg Ser Trp Gly Gln Pro			239
65	70	75	
GGG TAC CCT TGG CCC CTT TAC GCC AAT GAG GGC CTC GGG TGG GCA GGG Gly Tyr Pro Trp Pro Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly			287
80	85	90	95
TGG CTG CTC TCC CCT CGA GGC TCT CGG CCT AAT TGG GGC CCC AAT GAC Trp Leu Leu Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp			335
100	105	110	
CCC CGG CGA AAA TCG CGT AAT TTG GGT AAG GTC ATC GAT ACC CTA ACG Pro Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr			383
115	120	125	
TGC GGA TTC GCC GAT CTC ATG GGG TAT ATC CCG CTC GTA GGC GGC CCC Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly Pro			431
130	135	140	
ATT GGG GGC GTC GCA AGG GCT CTC GCA CAC GGT GTG AGG GTC CTT GAG Ile Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu			479
145	150	155	
GAC GGG GTA AAC TAT GCA ACA GGG AAT TTA Asp Gly Val Asn Tyr Ala Thr Gly Asn Leu			509
160	165		

(2) INFORMATION FOR SEQ ID NO: 42:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 169 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn			
1	5	10	15
Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gln Ile Val Gly			
20	25	30	
Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Met Gly Val Arg Ala			
35	40	45	
Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro			
50	55	60	
Ile Pro Lys Ala Arg Gln Pro Thr Gly Arg Ser Trp Gly Gln Pro Gly			
65	70	75	80
Tyr Pro Trp Pro Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly Trp			

85

90

95

Leu Leu Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp Pro
 100 105 110

Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys
 115 120 125

Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly Pro Ile
 130 135 140

Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp
 145 150 155 160

Gly Val Asn Tyr Ala Thr Gly Asn Leu
 165

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: PC-2-6

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 3..509

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

CC ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA AGA AAC ACC	47
Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr	
1 5 10 15	
AAC CGT CGC CCA CAG GAC GTC AAG TTC CCG GGC GGT GGT CAG ATC GTT	95
Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gln Ile Val	
20 25 30	
GCC GGA GTT TAC TTG TTG CCG CGC AGG GGC CCT AGG ATG GGT GTG CGC	143
Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Met Gly Val Arg	
35 40 45	
GCG ACT CGG AAG ACT TCG GAA CGG TCG CAA CCC CGT GGA CGG CGT CAG	191
Ala Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln	
50 55 60	

CCT ATT CCC AAG GCG CGC CAG CCC ACG GGC CGG TCC TGG GGT CAA CCC Pro Ile Pro Lys Ala Arg Gln Pro Thr Gly Arg Ser Trp Gly Gln Pro	239
65 70 75	
 GGG TAC CCT TGG CCC CTT TAC GCC AAT GAG GGC CTC GGG TGG GCA GGG Gly Tyr Pro Trp Pro Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly	287
80 85 90 95	
 TGG CTG CTC TCC CCT CGA GGC TCT CGG CCT AAT TGG GGC CCC AAT GAC Trp Leu Leu Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp	335
100 105 110	
 CCC CGG CGA AAA TCG CGT AAT TTG GGT AAG GTC ATC GAT ACC CTA ACG Pro Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr	383
115 120 125	
 TGC GGA TTC GCC GAT CTC ATG GGG TAT ATC CCG CTC GTA GGC GGC CCC Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly Pro	431
130 135 140	
 ATT GGG GGC GTC GCA AGG GCT CTC GCA CAC GGT GTG AGG GTC CTT GAG Ile Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu	479
145 150 155	
 GAC GGG GTA AAC TAT GCA ACA GGG AAT TTA Asp Gly Val Asn Tyr Ala Thr Gly Asn Leu	509
160 165	

(2) INFORMATION FOR SEQ ID NO: 44:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

Met	Ser	Thr	Asn	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn	Thr	Asn
1				5						10				15	
Arg	Arg	Pro	Gln	Asp	Val	Lys	Phe	Pro	Gly	Gly	Gly	Gln	Ile	Val	Gly
				20				25					30		
Gly	Val	Tyr	Leu	Leu	Pro	Arg	Arg	Gly	Pro	Arg	Met	Gly	Val	Arg	Ala
					35			40				45			.
Thr	Arg	Lys	Thr	Ser	Glu	Arg	Ser	Gln	Pro	Arg	Gly	Arg	Arg	Gln	Pro
						50		55				60			
Ile	Pro	Lys	Ala	Arg	Gln	Pro	Thr	Gly	Arg	Ser	Trp	Gly	Gln	Pro	Gly
					65		70			75			80		
Tyr	Pro	Trp	Pro	Leu	Tyr	Ala	Asn	Glu	Gly	Leu	Gly	Trp	Ala	Gly	Trp
						85			90				95		

Leu Leu Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp Pro
 100 105 110
 Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys
 115 120 125
 Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly Pro Ile
 130 135 140
 Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp
 145 150 155 160
 Gly Val Asn Tyr Ala Thr Gly Asn Leu
 165

(2) INFORMATION FOR SEQ ID NO: 45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 580 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: PC-4-1

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..580

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

A ACG TGC GGA TTC GCC GAT CTC ATG GGG TAT ATC CCG CTC GTA GGC	46
Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly	
1 5 10 15	
GGC CCC ATT GGG GGC GTC GCA AGG GCT CTC GCA CAC GGT GTG AGG GTC	94
Gly Pro Ile Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val	
20 25 30	
CTT GAG GAC GGG GTA AAC TAT GCA ACA GGG AAT TTA CCC GGT TGC TCT	142
Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser	
35 40 45	
TTC TCT ATC TTT ATT CTT GCT CTT CTC TCG TGT CTG ACC GTT CCG GCC	190
Phe Ser Ile Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala	
50 55 60	
TCT GCA GTT CCC TAC CGA AAT GCC TCT GGG ATT TAT CAT GTT ACC AAT	238

Ser Ala Val Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn			
65	70	75	
GAT TGC CCA AAC TCT TCC ATA GTC TAT GAG GCA GAT AAC CTG ATC CTA		286	
Asp Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asn Leu Ile Leu			
80	85	90	95
CAC GCA CCT GGT TGC GTG CCT TGT GTC ATG ACA GGT AAT GTG AGT AGA		334	
His Ala Pro Gly Cys Val Pro Cys Val Met Thr Gly Asn Val Ser Arg			
100	105	110	
TGC TGG GTC CAA ATT ACC CCT ACA CTG TCA GCC CCG ACC CTC GGA GCA		382	
Cys Trp Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Leu Gly Ala			
115	120	125	
GTC ACG GCT CCT CTT CGG AGA GCC GTT GAC TAC CTA GCG GGA GGG GCT		430	
Val Thr Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala Gly Gly Ala			
130	135	140	
GCC CTC TGC TCC GCG TTA TAC GTA GGA GAC GCG TGT GGG GCA CTA TTC		478	
Ala Leu Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe			
145	150	155	
TTG GTA GGC CAA ATG TTC ACC TAT AGG CCT CGC CAG CAC GCT ACG GTG		526	
Leu Val Gly Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val			
160	165	170	175
CAG AAC TGC AAC TGT TCC ATT TAC AGT GGC CAT GTT ACC GGC CAC CGG		574	
Gln Asn Cys Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Arg			
180	185	190	
ATG GCA		580	
Met Ala			

(2) INFORMATION FOR SEQ ID NO: 46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly			
1	5	10	15
Pro Ile Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu			
20	25	30	
Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe			
35	40	45	
Ser Ile Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser			
50	55	60	

Ala Val Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp
 65 70 75 80
 Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asn Leu Ile Leu His
 85 90 95
 Ala Pro Gly Cys Val Pro Cys Val Met Thr Gly Asn Val Ser Arg Cys
 100 105 110
 Trp Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Leu Gly Ala Val
 115 120 125
 Thr Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala Gly Gly Ala Ala
 130 135 140
 Leu Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe Leu
 145 150 155 160
 Val Gly Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val Gln
 165 170 175
 Asn Cys Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Arg Met
 180 185 190

Ala

(2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 580 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: PC-4-5

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..580

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

A ACG TGC GGA TTC GCC GAT CTC ATG GGG TAT ATC CCG CTC GTA GGC
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly
 1 5 10 15

46

GGC CCC ATT GGG GGC GTC GCA AGG GCT CTC GCA CAC GGT GTG AGG GTC

94

Gly Pro Ile Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val	20	25	30	
CTT GAG GAC GGG GTA AAC TAT GCA ACA GGG AAT TTA CCC GGT TGC TCT				142
Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser	35	40	45	
TTC TCT ATC TTT ATT CTT GCT CTT CGT TGT CTG ACC GTT CCG GCC				190
Phe Ser Ile Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala	50	55	60	
TCT GCA GTT CCC TAC CGA AAT GCC TCT GGG ATT TAT CAT GTT ACC AAT				238
Ser Ala Val Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn	65	70	75	
GAT TGC CCA AAC TCT TCC ATA GTC TAT GAG GCA GAT AAC CTG ATC CTA				286
Asp Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asn Leu Ile Leu	80	85	90	95
CAC GCA CCT GGT TGC GTG CCT TGT GTC ATG ACA GGT AAT GTG AGT AGA				334
His Ala Pro Gly Cys Val Pro Cys Val Met Thr Gly Asn Val Ser Arg	100	105	110	
TGC TGG GTC CAA ATT ACC CCT ACA CTG TCA GCC CCG AGC CTC GGA GCA				382
Cys Trp Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Leu Gly Ala	115	120	125	
GTC ACG GCT CCT CTT CGG AGA GCC GTT GAC TAC CTA GCG GGA GGG GCT				430
Val Thr Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala Gly Gly Ala	130	135	140	
GCC CTC TGC TCC GCG TTA TAC GTC GGA GAC GCG TGT GGG GCA CTA TTC				478
Ala Leu Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe	145	150	155	
TTG GTA GGC CAA ATG TTC ACC TAT AGG CCT CGC CAG CAC GCT ACG GTG				526
Leu Val Gly Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val	160	165	170	175
CAG AAC TGC AAC TGT TCC ATT TAC AGT GGC CAT GTT ACC GGC CAC CGG				574
Gln Asn Cys Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Arg	180	185	190	
ATG GCA				580
Met Ala				

(2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear -

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly
1 5 10 15

Pro Ile Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu
20 25 30

Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe
35 40 45

Ser Ile Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser
50 55 60

Ala Val Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp
65 70 75 80

Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asn Leu Ile Leu His
85 90 95

Ala Pro Gly Cys Val Pro Cys Val Met Thr Gly Asn Val Ser Arg Cys
100 105 110

Trp Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Leu Gly Ala Val
115 120 125

Thr Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala Gly Gly Ala Ala
130 135 140

Leu Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe Leu
145 150 155 160

Val Gly Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val Gln
165 170 175

Asn Cys Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Arg Met
180 185 190

Ala

(2) INFORMATION FOR SEQ ID NO: 49:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 959 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
(B) CLONE: PC-3-4

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 3..959

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49.

CC ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA AGA AAC ACC	47
Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr	
1 5 10 15	
AAC CGT CGC CCA CAG GAC GTC AAG TTC CCG GGC GGT GGT CAG ATC GTT	95
Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gln Ile Val	
20 25 30	
GGC GGA GTT TAC TTG TTG CCG CGC AGG GGC CCT AGG ATG GGT GTG CGC	143
Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Met Gly Val Arg	
35 40 45	
GCG ACT CGG AAG ACT TCG GAA CGG TCG CAA CCC CGT GGA CGG CGT CAG	191
Ala Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln	
50 55 60	
CCT ATT CCC AAG GCG CGC CAG CCC ACG GGC CGG TCC TGG GGT CAA CCC	239
Pro Ile Pro Lys Ala Arg Gln Pro Thr Gly Arg Ser Trp Gly Gln Pro	
65 70 75	
GGG TAC CCT TGG CCC CTT TAC GCC AAT GAG GGC CTC GGG TGG GCA GGG	287
Gly Tyr Pro Trp Pro Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly	
80 85 90 95	
TGG CTG CTC TCC CCT CGA GGC TCT CGG CCT AAT TGG GGC CCC AAT GAC	335
Trp Leu Leu Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp	
100 105 110	
CCC CGG CGA AAA TCG CGT AAT TTG GGT AAG GTC ATC GAT ACC CTA ACG	383
Pro Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr	
115 120 125	
TGC GGA TTC GCC GAT CTC ATG GGG TAT ATC CCG CTC GTA GGC GGC CCC	431
Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Pro	
130 135 140	
ATT GGG GGC GTC GCA AGG GCT CTC GCA CAC GGT GTG AGG GTC CTT GAG	479
Ile Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu	
145 150 155	
GAC GGG GTA AAC TAT GCA ACA GGG AAT TTA CCC GGT TGC TCT TTC TCT	527
Asp Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser	
160 165 170 175	
ATC TTT ATT CTT GCT CTT CTC TCG TGT CTG ACC GTT CCG GCC TCT GCA	575
Ile Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala	
180 185 190	
GTT CCC TAC CGA AAT GCC TCT GGG ATT TAT CAT GTT ACC AAT GAT TGC	623
Val Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp Cys	
195 200 205	

CCA AAC TCT TCC ATA GTC TAT GAG GCA GAT AAC CTG ATC CTA CAC GCA Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asn Leu Ile Leu His Ala 210 215 220	671
CCT GGT TGC GTG CCT TGT GTC ATG ACA GGT AAT GTG AGT AGA TGC TGG Pro Gly Cys Val Pro Cys Val Met Thr Gly Asn Val Ser Arg Cys Trp 225 230 235	719
GTC CAA ATT ACC CCT ACA CTG TCA GCC CCG AGC CTC GGA GCA GTC ACG Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Leu Gly Ala Val Thr 240 245 250 255	767
GCT CCT CTT CGG AGA GCC GTT GAC TAC CTA GCG GCA GGG GCT GCC CTC Ala Pro Leu Arg Ala Val Asp Tyr Leu Ala Gly Gly Ala Ala Leu 260 265 270	815
TGC TCC GCG TTA TAC GTA GGA GAC GCG TGT GGG GCA CTA TTC TTG GTA Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe Leu Val 275 280 285	863
GGC CAA ATG TTC ACC TAT AGG CCT CGC CAG CAC GCT ACG GTG CAG AAC Gly Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val Gln Asn 290 295 300	911
TGC AAC TGT TCC ATT TAC AGT GGC CAT GTT ACC GGC CAC CGG ATG GCA Cys Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Arg Met Ala 305 310 315	959

(2) INFORMATION FOR SEQ ID NO: 50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn 1 5 10 15
Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly 20 25 30
Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Met Gly Val Arg Ala 35 40 45
Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro 50 55 60
Ile Pro Lys Ala Arg Gln Pro Thr Gly Arg Ser Trp Gly Gln Pro Gly 65 70 75 80
Tyr Pro Trp Pro Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly Trp 85 90 95

Leu Leu Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp Pro
100 105 110

Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys
115 120 125

Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly Pro Ile
130 135 140

Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp
145 150 155 160

Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile
165 170 175

Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Val
180 185 190

Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp Cys Pro
195 200 205

Asn Ser Ser Ile Val Tyr Glu Ala Asp Asn Leu Ile Leu His Ala Pro
210 215 220

Gly Cys Val Pro Cys Val Met Thr Gly Asn Val Ser Arg Cys Trp Val
225 230 235 240

Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Leu Gly Ala Val Thr Ala
245 250 255

Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala Gly Gly Ala Ala Leu Cys
260 265 270

Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe Leu Val Gly
275 280 285

Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val Gln Asn Cys
290 295 300

Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Arg Met Ala
305 310 315

(2) INFORMATION FOR SEQ ID NO: 51:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 959 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: PC-3-8

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 3..959

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

CC ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA AGA AAC ACC	47
Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr	
1 5 10 15	
AAC CGT CGC CCA CAG GAC GTC AAG TTC CCG GGC GGT GGT CGG ATC GTT	95
Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gln Ile Val	
20 25 30	
Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Met Gly Val Arg	143
35 40 45	
GCG ACT CGG AAG ACT TCG GAA CGG TCG CAA CCC CGT GGA CGG CGT CAG	191
Ala Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln	
50 55 60	
CCT ATT CCC AAG GCG CGC CAG CCC ACG GGC CGG TCC TGG GGT CAA CCC	239
Pro Ile Pro Lys Ala Arg Gln Pro Thr Gly Arg Ser Trp Gly Gln Pro	
65 70 75	
GGG TAC CCT TGG CCC CTT TAC GCC AAT GAG GGC CTC GGG TGG GCA GGG	287
Gly Tyr Pro Trp Pro Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly	
80 85 90 95	
TGG CTG CTC CCT CGA GGC TCT CGG CCT AAT TGG GGC CCC AAT GAC	335
Trp Leu Leu Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp	
100 105 110	
CCC CGG CGA AAA TCG CGT AAT TTG GGT AAG GTC ATC GAT ACC CTA ACG	383
Pro Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr	
115 120 125	
TGC GGA TTC GCC GAT CTC ATG GGG TAC ATC CCG CTC GTA GGC GGC CCC	431
Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly Pro	
130 135 140	
GTT GGG GGC GTC GCA AGG GCT CTC GCA CAC GGT GTG AGG GTC CTT GAG	479
Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu	
145 150 155	
GAC GGG GTA AAC TAT CCA ACA GGG AAT TTA CCC GGT TGC TCT TTC TCT	527
Asp Gly Val Asn Tyr Pro Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser	
160 165 170 175	
ATC TTT ATT CTT GCT CTT CTC TCG TGT CTG ACC GTT CCG GCC TCT GCA	575
Ile Phe Ile Leu Ala Leu Ser Cys Leu Thr Val Pro Ala Ser Ala	
180 185 190	
GTT CCC TAC CGA AAT GCC TCT GGG ATT TAT CAT GTT ACC AAT GAT TGC	623

Val Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp Cys			
195	200	205	
CCA AAC TCT TCC ATA GTC TAT GAG GCA GAT AAC CTG ATC CTA CAC GCA			671
Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asn Leu Ile Leu His Ala			
210	215	220	
CCT GGT TGC GTG CCT TGT GTC ATG ACA GGT AAT GTG AGT AGA TGC TGG			719
Pro Gly Cys Val Pro Cys Val Met Thr Gly Asn Val Ser Arg Cys Trp			
225	230	235	
GTC CAA ATT ACC CCT ACA CTG TCA GCC CCG AGC CTC GGA GCA GTC ACG			767
Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Leu Gly Ala Val Thr			
240	245	250	255
GCT CCT CTT CGG AGA GCC GTT GAC TAC CTA GCG GGA GGG GCT GCC CTC			815
Ala Pro Leu Arg Ala Val Asp Tyr Leu Ala Gly Gly Ala Ala Leu			
260	265	270	
TGC TCC GCG TTA TAC GTA GGA GAC GCG TGT GGG GCA CTA TTC TTG GTA			863
Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe Leu Val			
275	280	285	
GGC CAA ATG TTC ACC TAT AGG CCT CGC CAG CAC GCT ACG GTG CAG AAC			911
Gly Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val Gln Asn			
290	295	300	
TGC AAC TGT TCC ATT TAC AGT GGC CAT GTT ACC GGC CAC CGG ATG GCA			959
Cys Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Arg Met Ala			
305	310	315	

(2) INFORMATION FOR SEQ ID NO: 52:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 319 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn			
1	5	10	15
Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly			
20	25	30	
Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Met Gly Val Arg Ala			
35	40	45	
Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro			
50	55	60	
Ile Pro Lys Ala Arg Gln Pro Thr Gly Arg Ser Trp Gly Gln Pro Gly			
65	70	75	80

Tyr Pro Trp Pro Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly Trp
85 90 95

Leu Leu Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp Pro
100 105 110

Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys
115 120 125

Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly Pro Val
130 135 140

Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp
145 150 155 160

Gly Val Asn Tyr Pro Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile
165 170 175

Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Val
180 185 190

Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp Cys Pro
195 200 205

Asn Ser Ser Ile Val Tyr Glu Ala Asp Asn Leu Ile Leu His Ala Pro
210 215 220

Gly Cys Val Pro Cys Val Met Thr Gly Asn Val Ser Arg Cys Trp Val
225 230 235 240

Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Leu Gly Ala Val Thr Ala
245 250 255

Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala Gly Gly Ala Ala Leu Cys
260 265 270

Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe Leu Val Gly
275 280 285

Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val Gln Asn Cys
290 295 300

Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Arg Met Ala
305 310 315

(2) INFORMATION FOR SEQ ID NO: 53:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 959 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: PC C/E1

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..959

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

CCATGAGCAC	GAATCCTAAA	CCTCAAAGAA	AAACCAAAG	AACACCAAC	CGTCGCCAC	60
AGGACGTCAA	GTTCCCCGGC	GGTGGTCAGA	TCGTTGGCGG	AGTTTACTTG	TTGCCGCGCA	120
GGGGCCCTAG	GATGGGTGTG	CGCGCGACTC	GGAAGACTTC	GGAACGGTGG	CAACCCCGTG	180
GACGGCGTCA	GCCTATTCCC	AAGGCAGGCC	AGCCCACGGG	CCGGTCCTGG	GTCAAACCGG	240
GCTACCCCTTG	GCCCCTTTAC	GCCAAATGAGG	GCCTCGGGTG	GGCAGGGTGG	CTGCTCTCCC	300
CTCGAGGCTC	TGGGCCTAAC	TGGGGCCCCA	ATGACCCCCG	GCGAAAATCG	CGTAATTGG	360
GTAAGGTCAT	CGATAACCCA	ACGTGCGGAT	TCGCGATCT	CATGGGGTAY	ATCCCCTCG	420
TAGGCAGGCC	CTTTGGGGGC	GTCGCAAGGG	CTCTCGCACA	CGGTGTGAGG	GTCCTTGAGG	480
ACGGGGTAAA	CTATSCAACCA	GGGAATTTCAC	CCGGTTGCTC	TTTCTCTATC	TTTATTCTTG	540
CTCTTCTCTC	GTGTCTGACC	GTTCGGGCCT	CTGCAGTTCC	CTACCGAAAT	GCCTCTGGGA	600
TTTATCATGT	TACCAATGAT	TGCCAAACT	CTTCCATAGT	CTATGAGGCA	GATAACCTGA	660
TCCTACACGC	ACCTGGTTGC	GTGCCCTGTG	TCATGACAGG	TAATGTGAGT	AGATGCTGGG	720
TCCAAATTAC	CCCTACACTG	TCAGCCCCGA	GCCTCGGAGC	AGTCACGGCT	CCTCTCGGA	780
GAGCCGTTGA	CTACCTAGCG	GGAGGGGCTG	CCCTCTGCTC	CGCGTTATAC	GTAGGAGACG	840
CGTGTGGGGC	ACTATTCTTG	GTAGGCCAAA	TGTTCACCTA	TAGGCCTCGC	CAGCACGCTA	900
CGGTGCAGAA	CTGCAACTGT	TCCATTACAA	GTGGCCATGT	TACCGGCCAC	CGGATGGCA	959

(2) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

Met	Ser	Thr	Asn	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn	Thr	Asn	
1																
							5							10		15

Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gln Ile Val Gly
 20 25 30

Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Met Gly Val Arg Ala
 35 40 45

Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro
 50 55 60

Ile Pro Lys Ala Arg Gln Pro Thr Gly Arg Ser Trp Gly Gln Pro Gly
 65 70 75 80

Tyr Pro Trp Pro Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly Trp
 85 90 95

Leu Leu Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp Pro
 100 105 110

Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys
 115 120 125

Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly Pro Val
 130 135 140

Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp
 145 150 155 160

Gly Val Asn Tyr Pro Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile
 165 170 175

Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Val
 180 185 190

Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp Cys Pro
 195 200 205

Asn Ser Ser Ile Val Tyr Glu Ala Asp Asn Leu Ile Leu His Ala Pro
 210 215 220

Gly Cys Val Pro Cys Val Met Thr Gly Asn Val Ser Arg Cys Trp Val
 225 230 235 240

Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Leu Gly Ala Val Thr Ala
 245 250 255

Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala Gly Gly Ala Ala Leu Cys
 260 265 270

Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe Leu Val Gly
 275 280 285

Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val Gln Asn Cys
 290 295 300

Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Arg Met Ala
 305 310 315

(2) INFORMATION FOR SEQ ID NO: 55:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 354 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
 (B) CLONE: PC-1-37

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..354

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

ACCACCGGAG CTTCTATCAC ATACTCCACT TACGGCAAGT TCCTTGCTGA TGGAGGGTGT	60
TCAGGGCGCG CGCATGACGT GATCATATGC GACGAGTGCC ATTCCCGAGGA CGCCACCACC	120
ATTCTTGGGA TAGGCACTGT CCTTGACCAAG GCAGAGACGG CTGGAGCTAG GCTCGTCGTC	180
TTGGCCACGG NCACCCCTCC CGGCAGTGTG ACAACGCCCG ACCCCAACAT CGAGGAAGTG	240
GCCCTGCCTC AGGAGGGGGA GGTTCCCTTC TACGGCAGAG CCATTCCCCT TGCTTTATA	300
AAGGGTGGTA GGCATCTCAT CTTCTGCCAT TCCAAGAAAA ATTGTGATGA ACTC	354

(2) INFORMATION FOR SEQ ID NO: 56:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 118 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

Thr Thr Gly Ala Ser Ile Thr Tyr Ser Thr Tyr Gly Lys Phe Leu Ala			
1	5	10	15
Asp Gly Gly Cys Ser Gly Gly Ala His Asp Val Ile Ile Cys Asp Glu			
20	25	30	

Cys His Ser Gln Asp Ala Thr Thr Ile Leu Gly Ile Gly Thr Val Leu
 35 40 45
 Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu Val Val Leu Ala Thr Xaa
 50 55 60
 Thr Pro Pro Gly Ser Val Thr Thr Pro His Pro Asn Ile Glu Glu Val
 65 70 75 80
 Ala Leu Pro Gln Glu Gly Glu Val Pro Phe Tyr Gly Arg Ala Ile Pro
 85 90 95
 Leu Ala Phe Ile Lys Gly Gly Arg His Leu Ile Phe Cys His Ser Lys
 100 105 110
 Lys Asn Cys Asp Glu Leu
 115

(2) INFORMATION FOR SEQ ID NO: 57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NC

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: PC-1-48

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..354

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

ACCACCGGAG CTTCTATCAC ATACTCCACT TACGGCAAGT TCCTTGCTGA TGGAGGGTGT	60
TCAGGCGGCG CGTATGACGT GATCATATGC GACGAGTGCC ATTCCCAGGA CGCCACCRCC	120
ATTCTTGGGA TAGGCACGT CCTTGACCAAG GCAGAGACGG CTGGAGCTAG GCTCGTCGTC	180
TTGGNCACGG NCACCCCTCC CGGCAGTGTG ACAACGCCCC ACCCCAACAT CGAGGARGTG	240
GCCCTGCCCTC AGGAGGGGGA GGTTCCCTTC TACGGNAGAG CCATTCCCCT TGCTTTATA	300
AAGGGTGGTA GGCATCTCAT CTTCTGCCAT TCCAAGAAAA AATGTGATGA ACTT	354

(2) INFORMATION FOR SEQ ID NO: 58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

Thr Thr Gly Ala Ser Ile Thr Tyr Ser Thr Tyr Gly Lys Phe Leu Ala
1 5 10 15

Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp Val Ile Ile Cys Asp Glu
20 25 30

Cys His Ser Gln Asp Ala Thr Thr Ile Leu Gly Ile Gly Thr Val Leu
35 40 45

Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu Val Val Leu Xaa Thr Xaa
50 55 60

Thr Pro Pro Gly Ser Val Thr Thr Pro His Pro Asn Ile Glu Glu Val
65 70 75 80

Ala Leu Pro Gln Glu Gly Glu Val Pro Phe Tyr Xaa Arg Ala Ile Pro
85 90 95

Leu Ala Phe Ile Lys Gly Gly Arg His Leu Ile Phe Cys His Ser Lys
100 105 110

Lys Lys Cys Asp Glu Leu Arg Gln Ala Thr Asp Gln Pro Gly Arg Glu
115 120 125

Arg Pro Trp Glu Tyr
130

(2) INFORMATION FOR SEQ ID NO: 59:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 357 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: PC-1-37

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..357

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

ATGGCTTCATGTCTCCGGA CTTGGAGGTC ATTACCA	60
CTTGGTTCT GGTGGGGGGC	
GTTGTGGCGA CCCTGCNCCTACTGCTTG ACGGTGGTT CGGTAGCCAT AGTCGGTAGG	120
ATCATCCTCT CTGGAAACC TGCCATCATT NCCGATAGGG AGGTATTATA CCAGCAATT	180
GATGAGATGG AGGAGTGCTC GGCCTCGTTG CCCTATATGG ACGAAACACG TNCCATTGCC	240
GGACAATTCA AAGAGAAAAGT GCTCGGCTTC ATCAGCACGA CCGGCCAGAA GGCTGAAACT	300
CTGAAGCCGG CAGCCACGTC TGTGTGGAAC AAGGCTGATC AGTTCTGGNC CACATAC	357

(2) INFORMATION FOR SEQ ID NO: 60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

Met Ala Phe Met Ser Pro Asp Leu Glu Val Ile Thr Xaa Thr Trp Val			
1	5	10	15
Leu Val Gly Val Val Ala Thr Leu Xaa Xaa Tyr Cys Leu Thr Val			
20	25	30	
Gly Ser Val Ala Ile Val Gly Arg Ile Ile Leu Ser Gly Lys Pro Ala			
35	40	45	
Ile Ile Xaa Asp Arg Glu Val Leu Tyr Gln Gln Phe Asp Glu Met Glu			
50	55	60	
Glu Cys Ser Ala Ser Leu Pro Tyr Met Asp Glu Thr Arg Xaa Ile Ala			
65	70	75	80
Gly Gln Phe Lys Glu Lys Val Leu Gly Phe Ile Ser Thr Thr Gly Gln			
85	90	95	
Lys Ala Glu Thr Leu Lys Pro Ala Ala Thr Ser Val Trp Asn Lys Ala			
100	105	110	
Asp Gln Phe Trp Xaa Thr Tyr Met Trp Asn Phe Ile Ser Gly Ile Gln			
115	120	125	

(2) INFORMATION FOR SEQ ID NO: 61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: PC-1-48

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..357

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

ATGGCTTGCA TGTCTGCGGA CCTGGAGGTC ATTACCANCA CTTGGGTTCT GGTGGGGGGC	60
GTTGTGGCGN CCCTGGCGGC CTACTGCTTG ACGGTGGGTT CGGTAGCCAT AGTCGGTAGG	120
ATCATCCTCT CTGGGAAACC TGCCATCATT CCCGATAGGG AGGCATTATA CCANCAATT	180
GATGAGATGG AGGAGTGCTC GGCCTCGTTG CCCTATATGG ACGAGACACG TGCCATTGCC	240
GGACRAATTCA AAGAGAAAAGT GCTCGGCTTC ATCAGCACGA CCGGCCAGAA GGCTGAAACT	300
CTGAAGCCGG CAGCCACGTC TGTGTGGAAC AAGGCTGANC AGTTCTGGGC CACATAC	357

(2) INFORMATION FOR SEQ ID NO: 62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

Met Ala Cys Met Ser Ala Asp Leu Glu Val Ile Thr Xaa Thr Trp Val			
1	5	10	15
Leu Val Gly Gly Val Val Ala Xaa Leu Ala Ala Tyr Cys Leu Thr Val			
20	25	30	
Gly Ser Val Ala Ile Val Gly Arg Ile Ile Leu Ser Gly Lys Pro Ala			
35	40	45	
Ile Ile Pro Asp Arg Glu Ala Leu Tyr Xaa Gln Phe Asp Glu Met Glu			
50	55	60	

Glu Cys Ser Ala Ser Leu Pro Tyr Met Asp Glu Thr Arg Ala Ile Ala
 65 70 75 80

Gly Gln Phe Lys Glu Lys Val Leu Gly Phe Ile Ser Thr Thr Gly Gln
 85 90 95

Lys Ala Glu Thr Leu Lys Pro Ala Ala Thr Ser Val Trp Asn Lys Ala
 100 105 110

Xaa Gln Phe Trp Ala Thr Tyr Met Trp Asn Phe Ile Ser Gly Ile Gln
 115 120 125

(2) INFORMATION FOR SEQ ID NO: 63:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /standard_name= "HCV Primer HCPr161"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

ACCGGAGGCC AGGAGAGTGA TCTCCTCC

28

(2) INFORMATION FOR SEQ ID NO: 64:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: YES

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /standard_name= "HCV Primer HCPr162"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

GGGCTGCTCT ATCCTCATCG ACGCCATC

28

(2) INFORMATION FOR SEQ ID NO: 65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /standard_name= "HCV Primer HCPr163"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

GCCAGAGGCT CGGAAGGCGA TCAGCGCT

28

(2) INFORMATION FOR SEQ ID NO: 66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: YES

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /standard_name= "HCV Primer HCPr164"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

GAGCTGCTCT GTCCCTCTCG ACGCCGCA

28

(2) INFORMATION FOR SEQ ID NO: 67:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /standard_name= "HCV Primer HCPr23"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

CTCATGGGGT ACATTCCGCT

20

(2) INFORMATION FOR SEQ ID NO: 68:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: YES

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /standard_name= "HCV Primer HCPr54"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

CTATTACCA G TTCATCATCA TATCCCA

27

(2) INFORMATION FOR SEQ ID NO: 69:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /standard_name= "HCV Primer HCPr116"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

TTTTAAATAC ATCATGRCTG YATG

24

(2) INFORMATION FOR SEQ ID NO: 70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: YES

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /standard_name= "HCV Primer HCPr66"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

CTATTATTGT ATCCRCTGA TGAARTTCCA CAT

33

(2) INFORMATION FOR SEQ ID NO: 71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: YES

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

- (B) LOCATION: 1..28
(D) OTHER INFORMATION: /standard_name= "HCV Primer
HCPr118:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

ACTAGTCGAC TAYTGATCCR CTATRWARTT CCACAT

36

(2) INFORMATION FOR SEQ ID NO: 72:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION: 1..28
(D) OTHER INFORMATION: /standard_name= "HCV Primer
HCPr117:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

TTTTAAATAC ATCGCRTGC ATGCA

25

(2) INFORMATION FOR SEQ ID NO: 73:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: YES

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION: 1..28
(D) OTHER INFORMATION: /standard_name= "HCV Primer
HCPr119:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

ACTAGTCGAC TARTTGCATA GCCKRTTCAT CCAYTG

36

(2) INFORMATION FOR SEQ ID NO: 74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /standard_name= "HCV Primer HCPr131:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

GGAATTCTAG ACCTCTGGGA YGARAYTGGAA ARTG

34

(2) INFORMATION FOR SEQ ID NO: 75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /standard_name= "HCV Primer HCPr130:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

GGAATTCTAG ACGCTAYCAR GCACGTTGYG C

31

(2) INFORMATION FOR SEQ ID NO: 76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /standard_name= "HCV Primer
HCPr134:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

CATATAGATG CCCACTTCCT ATC

23

(2) INFORMATION FOR SEQ ID NO: 77:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 16 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: YES

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /standard_name= "HCV Primer
HCPr3:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

GTGTGCCAGG ACCATC

16

(2) INFORMATION FOR SEQ ID NO: 78:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: YES

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /standard_name= "HCV Primer HCPr4:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

GACATGCATG TCATGATGTA

20

(2) INFORMATION FOR SEQ ID NO: 79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /standard_name= "HCV Primer HCPr152:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

TACGCCCTCTT CTATATCGGT TGGGGCCTG

29

(2) INFORMATION FOR SEQ ID NO: 80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /standard_name= "HCV Primer HCPr52;

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

ATGTTGGGTA AGGTCAATCGA TACCCCT

26

(2) INFORMATION FOR SEQ ID NO: 81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /standard_name= "HCV Primer HCPr41;

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

CCCGGGAGGT CTCGTAGACC GTGCA

25

(2) INFORMATION FOR SEQ ID NO: 82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: YES

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /standard_name= "HCV Primer HCPr40;

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

CTATTAAGA TAGAGAAAGA GCAACCGGG

29

(1) INFORMATION FOR SEQ ID NO: 83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN PROTEIN:

(B) MAP POSITION: positions 192 to 203 of the V1 region of HCV
type 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN PROTEIN:

(B) MAP POSITION: positions 192 to 203 of the V1 region of HCV
type 5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

Val Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN PROTEIN:

(B) MAP POSITION: positions 213 to 223 of the V2 region of HCV
type 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

Val Tyr Glu Ala Asp Asp Val Ile Leu His Thr
1 5 10

(2) INFORMATION FOR SEQ ID NO: 86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN PROTEIN:

(B) MAP POSITION: positions 213 to 233 of the V2 region of HCV
type 5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

Val Tyr Glu Ala Asp Asn Leu Ile Leu His Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO: 87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN PROTEIN:

(B) MAP POSITION: positions 230 to 242 of the V3 region of HCV
type 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

Val Gln Asp Gly Asn Thr Ser Thr Cys Trp Thr Pro Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN PROTEIN:

(B) MAP POSITION: positions 230 to 242 of the V3 region of HCV
type 5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

Val Met Thr Gly Asn Val Ser Arg Cys Trp Val Gln Ile
1 5 10

(2) INFORMATION FOR SEQ ID NO: 89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN PROTEIN:

(B) MAP POSITION: positions 248 to 257 of the V4 region of HCV
type 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

Val Arg Tyr Val Gly Ala Thr Thr Ala Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO: 90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN PROTEIN:

(B) MAP POSITION: positions 248 to 257 of the V4 region of HCV
type 5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

Ala Pro Ser Leu Gly Ala Val Thr Ala Pro
1 5 10

(2) INFORMATION FOR SEQ ID NO: 91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN PROTEIN:

(B) MAP POSITION: positions 294 to 303 of the V5 region of HCV
type 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

Arg Pro Arg Arg His Gln Thr Val Gln Thr
1 5 10

(2) INFORMATION FOR SEQ ID NO: 92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN PROTEIN:

(B) MAP POSITION: positions 294 to 303 of the V5 region of HCV
type 5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

Arg Pro Arg Gln His Ala Thr Val Gln Asn
1 5 10

(2) INFORMATION FOR SEQ ID NO: 93:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN PROTEIN:

(B) MAP POSITION: positions 70 to 78 of HCV type 5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

Gln Pro Thr Gly Arg Ser Trp Gly Gln
1 5

(2) INFORMATION FOR SEQ ID NO: 94:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: BR33 and BR36

(viii) POSITION IN PROTEIN:

(B) MAP POSITION: positions 230 to 237 of the V3 region of HCV
type 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

Val Gln Asp Gly Asn Thr Ser Thr
1 5

(2) INFORMATION FOR SEQ ID NO: 95:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: HD10

(viii) POSITION IN PROTEIN:

(B) MAP POSITION: positions 230 to 237 of the V3 region of HCV
type 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

Val Gln Asp Gly Asn Thr Ser Ala
1 5

(2) INFORMATION FOR SEQ ID NO: 96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: BR36

(viii) POSITION IN PROTEIN:

(B) MAP POSITION: positions 248 to 257 of the V4 region of HCV
type 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

Val Lys Tyr Val Gly Ala Thr Thr Ala Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO: 97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: BR36

(viii) POSITION IN GENOME:

(B) MAP POSITION: Positions 1688 to 1707 of HCV type 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87.

Leu Gly Gly Lys Pro Ala Ile Val Pro Asp Lys Glu Val Leu Tyr Gln
 1 5 10 15
 Gln Tyr Asp Glu
 20

(2) INFORMATION FOR SEQ ID NO: 88.

(i) SEQUENCE CHARACTERISTICS

SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: HD10

(viii) POSITION IN GENOME.

(B) MAP POSITION: positions 1688 to 1703 of UGM, type 3

(xi) SEQUENCE DESCRIPTION SEQ ID NO: 3

Leu Gly Gly Lys Pro Ala Leu Val Pro Asp Lys Glu Val Leu Tyr Gln
 1 5 10 15
 Gln Tyr Asp Glu
 20

(2) INFORMATION FOR SEQ ID NO: 22

(i) SEQUENCE CHARACTERISTICS

SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptides

(iii) HYPOTHETICAL: NO

(iii) POSITION IN GROUP

(B) MAP POSITION: *lacc* (laccase)

(iii) SOURCE READING

Ser Gln Ala Ala Pro Tyr Ile Glu Gln Ala Gln Val Ile Ala His Gln
1 5 10 15

Phe Lys Glu Lys
20

(2) INFORMATION FOR SEQ ID NO: 100:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: BR36

(viii) POSITION IN GENOME:

(B) MAP POSITION: positions 1724 to 1743 of HCV type 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

Ile Ala His Gln Phe Lys Glu Lys Val Leu Gly Leu Leu Gln Arg Ala
1 5 10 15

Thr Gln Gln Gln
20

(2) INFORMATION FOR SEQ ID NO: 101:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: HD10

(viii) POSITION IN GENOME:

(B) MAP POSITION: positions 1724 to 1743 of HCV type 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

Ile Ala His Gln Phe Lys Glu Lys Ile Leu Gly Leu Leu Gln Arg Ala
1 5 10 15

Thr Gln Gln Gln
20

(2) INFORMATION FOR SEQ ID NO: 102:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN GENOME:

(B) MAP POSITION: positions 1688 to 1707 of HCV type 5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

Leu Ser Gly Lys Pro Ala Ile Ile Pro Asp Arg Glu Ala Leu Tyr Gln
1 5 10 15

Gln Phe Asp Glu
20

(2) INFORMATION FOR SEQ ID NO: 103:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN GENOME:

(B) MAP POSITION: positions 1688 to 1707

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

Leu Ser Gly Lys Pro Ala Ile Ile Pro Asp Arg Glu Val Leu Tyr Gln
1 5 10 15

Gln Phe Asp Glu
20

(2) INFORMATION FOR SEQ ID NO: 104:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN GENOME:

(B) MAP POSITION: position 1712 to 1731 of HCV type 5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

Ser	Ala	Ser	Leu	Pro	Tyr	Met	Asp	Glu	Thr	Arg	Ala	Ile	Ala	Gly	Gln
1															15
Phe	Lys	Glu	Lys												
				20											

(2) INFORMATION FOR SEQ ID NO: 105:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN GENOME:

(B) MAP POSITION: positions 1724 to 1743 of HCV type 5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

Ile	Ala	Gly	Gln	Phe	Lys	Glu	Lys	Val	Leu	Gly	Phe	Ile	Ser	Thr	Thr
1															15
Gly	Gln	Lys	Ala												
				20											

(2) INFORMATION FOR SEQ ID NO: 106:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 340 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: GB48-3-10

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

C TCC ACT GTA ACC GAA AAG GAC ATC AGG GTC GAG GAG GTC TAT	46
Ser Thr Val Thr Glu Lys Asp Ile Arg Val Glu Glu Glu Val Tyr	
1 5 10 15	
 CAG TGT TGT GAC CTG GAG CCC GAA GCC CGC AAG GCA ATT ACC GCC CTA	94
Gln Cys Cys Asp Leu Glu Pro Ala Arg Lys Ala Ile Thr Ala Leu	
20 25 30	
 ACA GAG AGA CTC TAC GTG GGC GGT CCC ATG CAT AAC AGC AAG GGA GAC	142
Thr Glu Arg Leu Tyr Val Gly Gly Pro Met His Asn Ser Lys Gly Asp	
35 40 45	
 CTG TGC GGG TAT CGC AGA TGT CGC GCA AGC GGC GTC TAC ACC ACC AGC	190
Leu Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser	
50 55 60	
 TTC GGG AAC ACA CTG ACG TGC TAC CTC AAA GCC TCA GCC GCT ATC AAA	238
Phe Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Ile Lys	
65 70 75	
 GCG GCG GGG CTG AGA GAC TGC ACC ATG TTG GTC TGT GGT GAT GAC CTG	286
Ala Ala Gly Leu Arg Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu	
80 85 90 95	
 GTT GTC ATC GCT GAG AGC GAT GGC GTA GAG GAG GAC AAA CGA CCC CTC	334
Val Val Ile Ala Glu Ser Asp Gly Val Glu Glu Asp Lys Arg Pro Leu	
100 105 110	
 GGA GCC	340
Gly Ala	

(2) INFORMATION FOR SEQ ID NO: 107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

Ser Thr Val Thr Glu Lys Asp Ile Arg Val Glu Glu Glu Val Tyr Gln	
1 5 10 15	

Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Ala Ile Thr Ala Leu Thr
 20 25 30

 Glu Arg Leu Tyr Val Gly Gly Pro Met His Asn Ser Lys Gly Asp Leu
 35 40 45

 Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser Phe
 50 55 60

 Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Ile Lys Ala
 65 70 75 80

 Ala Gly Leu Arg Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val
 85 90 95

 Val Ile Ala Glu Ser Asp Gly Val Glu Glu Asp Lys Arg Pro Leu Gly
 100 105 110

Ala

(2) INFORMATION FOR SEQ ID NO: 108:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 340 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: GB116-3-5

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 2..340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

C TCC ACT GTA ACC GAA AAG GAC ATC AGG GTC GAG GAG GAG GTA TAT	46
Ser Thr Val Thr Glu Lys Asp Ile Arg Val Glu Glu Val Tyr	
1 5 10 15	
CAG TGT TGT GAC CTG GAG CCC GAG GCC CGC AGA GCA ATT ACC GCC CTA	94
Gln Cys Cys Asp Leu Glu Pro Glu Ala Arg Arg Ala Ile Thr Ala Leu	
20 25 30	
ACA GAG AGA CTC TAC GTG GGC GGT CCC ATG CAT AAC AGC AGG GGA GAC	142
Thr Glu Arg Leu Tyr Val Gly Gly Pro Met His Asn Ser Arg Gly Asp	
35 40 45	

172

CTG TGC GGG TAT CGC AGA TGC CGT GCG AGC GGC GTC TAC ACC ACC AGC		190	
Leu Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser			
50	55	60	
TTC GGG AAC ACA CTG ACG TGC TAT CTC AAA GCC TCA GCC GCT ATC AGA		238	
Phe Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Ile Arg			
65	70	75	
GCG GCG GGG CTG AGA GAC TGC ACC ATG TTG GTC TGT GGT GAT GAC CTG		286	
Ala Ala Gly Leu Arg Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu			
80	85	90	95
GTC GTC ATT GCT GAA AGC GAT GGC GTA GAG GAG GAC AAA CGA GCC CTC		334	
Val Val Ile Ala Glu Ser Asp Gly Val Glu Glu Asp Lys Arg Ala Leu			
100	105	110	
GGA GCC		340	
Gly Ala			

(2) INFORMATION FOR SEO ID NO: 109:

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

) MOLECULE TYPE: protein

) SEQUENCE DESCRIPTION: SEQ ID NO: 109

Ser Thr Val Thr Glu Lys Asp Ile Arg Val Glu Glu Glu Val Tyr Gln
 1 5 10 15

Cys Cys Asp Leu Glu Pro Glu Ala Arg Arg Ala Ile Thr Ala Leu Thr
 20 25 30

Glu Arg Leu Tyr Val Gly Gly Pro Met His Asn Ser Arg Gly Asp Leu
 35 40 45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser Phe
 50 55 60

Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Ile Arg Ala
 65 70 75 80

Ala Gly Leu Arg Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val
 85 90 95

Val Ile Ala Glu Ser Asp Gly Val Glu Glu Asp Lys Arg Ala Leu Gly
 100 105 110

Ala

(2) INFORMATION FOR SEQ ID NO: 110:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: GB215-3-8

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

C TCC ACT GTA ACC GAA AAA GAC ATC AGG GTC GAG GAG GAG GTA TAT	46
Ser Thr Val Thr Glu Lys Asp Ile Arg Val Glu Glu Glu Val Tyr	
1 5 10 15	
CAG TGT TGT GAC CTG GAG CCC GAA GCC CGC AAG GTA ATT ACC GCC CTA	94
Gln Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Thr Ala Leu	
20 25 30	
ACA GAG AGA CTC TAT GTG GGC GGT CCC ATG CAT AAT AGC AAA GGA GAC	142
Thr Glu Arg Leu Tyr Val Gly Gly Pro Met His Asn Ser Lys Gly Asp	
35 40 45	
CTG TGC GGG TAT CGC AGA TGC CGC GCA AGC GGC GTC TAC ACC ACC AGC	190
Leu Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser	
50 55 60	
TTC GGG AAC ACA CTG ACG TGC TAT CTC AAA GCC TCA GCC GCC ATC AGG	238
Phe Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Ile Arg	
65 70 75	
GCG TCA GGG CTG AGA GAC TGC ACT ATG CTG GTC TAT GGT GAC GAC CTG	286
Ala Ser Gly Leu Arg Asp Cys Thr Met Leu Val Tyr Gly Asp Asp Leu	
80 85 90 95	
GTC GTC ATT GCC GAG AGC GAT GGC GTA GAG GAG GAC AAA CGA GCC CTC	334
Val Val Ile Ala Glu Ser Asp Gly Val Glu Glu Asp Lys Arg Ala Leu	
100 105 110	
GGA GTC	340
Gly Val	

(2) INFORMATION FOR SEQ ID NO: 111:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

Ser	Thr	Val	Thr	Glu	Lys	Asp	Ile	Arg	Val	Glu	Glu	Glu	Val	Tyr	Gln
1				5					10					15	

Cys	Cys	Asp	Leu	Glu	Pro	Glu	Ala	Arg	Lys	Val	Ile	Thr	Ala	Leu	Thr
			20					25				30			

Glu	Arg	Leu	Tyr	Val	Gly	Gly	Pro	Met	His	Asn	Ser	Lys	Gly	Asp	Leu
				35			40				45				

Cys	Gly	Tyr	Arg	Arg	Cys	Arg	Ala	Ser	Gly	Val	Tyr	Thr	Thr	Ser	Phe
					50		55			60					

Gly	Asn	Thr	Leu	Thr	Cys	Tyr	Leu	Lys	Ala	Ser	Ala	Ala	Ile	Arg	Ala
					65		70		75			80			

Ser	Gly	Leu	Arg	Asp	Cys	Thr	Met	Leu	Val	Tyr	Gly	Asp	Asp	Leu	Val
					85			90			95				

Val	Ile	Ala	Glu	Ser	Asp	Gly	Val	Glu	Glu	Asp	Lys	Arg	Ala	Leu	Gly
					100			105			110				

Val

(2) INFORMATION FOR SEQ ID NO: 112:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 340 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: GB358-3-3

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

C TCC ACT GTA ACC GAA AAG GAC ATC AGG GTC GAG GAG GTG TAT

175

Ser Thr Val Thr Glu Lys Asp Ile Arg Val Glu Glu Val Tyr					
1	5	10	15		
CAG TGT TGT GAC CTG GAG CCC GAG GCC CGC AAG GCA ATT ACT GCC CTA					94
Gln Cys Cys Asp Leu Glu Pro Ala Arg Lys Ala Ile Thr Ala Leu					
20	25	30			
ACA GAG AGA CTC TAT GTG GGC GGT CCC ATG CAT AAC AGC AAG GGA GAC					142
Thr Glu Arg Leu Tyr Val Gly Gly Pro Met His Asn Ser Lys Gly Asp					
35	40	45			
CTG TGT GGG TAT CGC AGA TGC CGC GCA AGC GGC GTC TAC ACC ACC AGC					190
Leu Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser					
50	55	60			
TTC GGG AAC ACA CTG ACG TGC TAC CTC AAA GCC TCA GCC GCT ATC AGA					238
Phe Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Ile Arg					
65	70	75			
GCG GCG GGG CTG AGA GAC TGC ACC ATG TTG GTC TGT GGT GAT GAC CTG					286
Ala Ala Gly Leu Arg Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu					
80	85	90	95		
GTC GTC ATC GCT GAG AGC GAT GGC GTT GAG GAG GAC AAA CGA GCC CTC					334
Val Val Ile Ala Glu Ser Asp Gly Val Glu Glu Asp Lys Arg Ala Leu					
100	105	110			
GGA GCC					340
Gly Ala					

(2) INFORMATION FOR SEQ ID NO: 113:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

Ser Thr Val Thr Glu Lys Asp Ile Arg Val Glu Glu Val Tyr Gln					
1	5	10	15		
Cys Cys Asp Leu Glu Pro Ala Arg Lys Ala Ile Thr Ala Leu Thr					
20	25	30			
Glu Arg Leu Tyr Val Gly Gly Pro Met His Asn Ser Lys Gly Asp Leu					
35	40	45			
Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser Phe					
50	55	60			
Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Ile Arg Ala					
65	70	75	80		

Ala Gly Leu Arg Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val
85 90 95

Val Ile Ala Glu Ser Asp Gly Val Glu Glu Asp Lys Arg Ala Leu Gly
100 105 110

Ala

(2) INFORMATION FOR SEQ ID NO: 114:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 340 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
 (B) CLONE: GB549-3-6

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 2..340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

C TCC ACG GTG ACC GAA AGG GAT ATC AGG ACC GAG GAA GAG ATC TAC	46
Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Glu Glu Ile Tyr	
1 5 10 15	
CAG TGC TGC GAC CTG GAG CCC GAA GCC CGC AAG GTG ATA TCC GCC CTA	94
Gln Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Ser Ala Leu	
20 25 30	
ACG GAA AGA CTC TAC GTG GGC GGT CCC ATG TAC AAC TCC AAG GGG GAC	142
Thr Glu Arg Leu Tyr Val Gly Gly Pro Met Tyr Asn Ser Lys Gly Asp	
35 40 45	
CTA TGC GGG CAA CGG AGG TGC CGC GCA AGC GGG GTC TAC ACC ACC AGC	190
Leu Cys Gly Gln Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser	
50 55 60	
TTC GGG AAC ACT GTA ACG TGT TAT CTC AAG GCC GTT GCG GCT ACT AGG	238
Phe Gly Asn Thr Val Thr Cys Tyr Leu Lys Ala Val Ala Ala Thr Arg	
65 70 75	
GCC GCA GGT CTG AAA GGT TGC AGC ATG CTG GTT TGT GGA GAC GAC TTA	286
Ala Ala Gly Leu Lys Gly Cys Ser Met Leu Val Cys Gly Asp Asp Leu	
80 85 90 95	

GTC GTC ATC TGC GAG AGC GGC GGC GTA GAG GAG GAT GCA AGA GCC CTC
 Val Val Ile Cys Glu Ser Gly Gly Val Glu Glu Asp Ala Arg Ala Leu
 100 105 110

334

CGA GCC
 Arg Ala

340

(2) INFORMATION FOR SEQ ID NO: 115:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Glu Glu Ile Tyr Gln
 1 5 10 15

Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Ser Ala Leu Thr
 20 25 30

Glu Arg Leu Tyr Val Gly Gly Pro Met Tyr Asn Ser Lys Gly Asp Leu
 35 40 45

Cys Gly Gln Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser Phe
 50 55 60

Gly Asn Thr Val Thr Cys Tyr Leu Lys Ala Val Ala Ala Thr Arg Ala
 65 70 75 80

Ala Gly Leu Lys Gly Cys Ser Met Leu Val Cys Gly Asp Asp Leu Val
 85 90 95

Val Ile Cys Glu Ser Gly Gly Val Glu Glu Asp Ala Arg Ala Leu Arg
 100 105 110

Ala

(2) INFORMATION FOR SEQ ID NO: 116:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 340 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
 (B) CLONE: GB809-3-1

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 2..340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

C TCC ACT GTG ACT GAG AGA GAC ATC AAG GTC GAA GAA GTC TAT	46
Ser Thr Val Thr Glu Arg Asp Ile Lys Val Glu Glu Val Tyr	
1 5 10 15	
 CAG TGT TGT GAT CTG GAG CCC GAG GCC CGC AAG GTA ATA GCC GCC CTC	94
Gln Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Ala Ala Leu	
20 25 30	
 ACG GAG AGA CTC TAC GTG GGC GGC CCC ATG CAT AAC AGC AAG GGA GAC	142
Thr Glu Arg Leu Tyr Val Gly Gly Pro Met His Asn Ser Lys Gly Asp	
35 40 45	
 CTT TGC GGG TAT CGT AGA TGC CGC GCG AGC GGC GTA TAC ACC ACC AGC	190
Leu Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser	
50 55 60	
 TTC GGG AAC ACA ATG ACG TGC TAC CTT AAG GCC TCA GCA GCC ATC AGG	238
Phe Gly Asn Thr Met Thr Cys Tyr Leu Lys Ala Ser Ala Ala Ile Arg	
65 70 75	
 GCT GCG GGG CTA AAG GAT TGC ACC ATG CTG GTT TGC GGT GAC GAC CTA	286
Ala Ala Gly Leu Lys Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu	
80 85 90 95	
 GTC GTG ATC GCC GAG AGC GGT GGC GTT GAG GAG GAC AAA CGA GCC CTC	334
Val Val Ile Ala Glu Ser Gly Gly Val Glu Glu Asp Lys Arg Ala Leu	
100 105 110	
 GGA GCT	340
Gly Ala	

(2) INFORMATION FOR SEQ ID NO: 117:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

Ser Thr Val Thr Glu Arg Asp Ile Lys Val Glu Glu Glu Val Tyr Gln	
1 5 10 15	

Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Ala Ala Leu Thr
 20 25 30

Glu Arg Leu Tyr Val Gly Gly Pro Met His Asn Ser Lys Gly Asp Leu
 35 40 45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser Phe
 50 55 60

Gly Asn Thr Met Thr Cys Tyr Leu Lys Ala Ser Ala Ala Ile Arg Ala
 65 70 75 80

Ala Gly Leu Lys Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val
 85 90 95

Val Ile Ala Glu Ser Gly Gly Val Glu Glu Asp Lys Arg Ala Leu Gly
 100 105 110

Ala

(2) INFORMATION FOR SEQ ID NO: 118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 574 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: GB358-4-1

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..574

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

ACT TGC GGC TTT GCC GAC CTC ATG GGA TAC ATC CCG CTC GTA GGC GCC 48
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala
 1 5 10 15

CCT GTG GGT GGC GTC GCC AGG GCC CTG GCA CAC GGT GTT AGG GCT GTG 96
 Pro Val Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val
 20 25 30

GAG GAC GGG ATC AAT TAT GCG ACA GGG AAT CTT CCC GGT TGC TCT TTC 144
 Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe
 35 40 45

180

TCT ATC TTC CTC TTG GCA CTT CTT TCG TGC CTG ACT GTT CCC ACC TCG Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Thr Ser	192
50 55 60	
GCC GTC AAC TAT CGC AAT GCC TCG GGC ATC TAT CAC ATC ACC AAT GAC Ala Val Asn Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile Thr Asn Asp	240
65 70 75 80	
TGC CCG AAC TCG AGC ATA GTG TAC GAG ACC GAG CAC CAC ATC CTA CAC Cys Pro Asn Ser Ser Ile Val Tyr Glu Thr Glu His His Ile Leu His	288
85 90 95	
CTC CCA GGG TGT TTA CCC TGC GTG AGG GTT GGG AAT CAG TCA CGC TGC Leu Pro Gly Cys Leu Pro Cys Val Arg Val Gly Asn Gln Ser Arg Cys	336
100 105 110	
TGG GTG GCC CTC ACT CCC ACC GTG GCG GCG CCT TAC ATC GGC GCT CCG Trp Val Ala Leu Thr Pro Thr Val Ala Ala Pro Tyr Ile Gly Ala Pro	384
115 120 125	
CTT GAA TCC CTC CGG AGT CAT GTG GAT CTG ATG GTA GGT GCC GCT ACT Leu Glu Ser Leu Arg Ser His Val Asp Leu Met Val Gly Ala Ala Thr	432
130 135 140	
GCG TGC TCC GCT CTT TAC ATC GGA GAC CTG TGC GGT GGC GTA TTC TTG Ala Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu	480
145 150 155 160	
GTT GGT CAG ATG TTC TCT TTC CAG CCG CGG CGC CAC TGG ACT ACG CAG Val Gly Gln Met Phe Ser Phe Gln Pro Arg Arg His Trp Thr Thr Gln	528
165 170 175	
GAC TGC AAT TGT TCC ATC TAC GCG GGG CAC GTT ACG GGC CAC AGG A Asp Cys Asn Cys Ser Ile Tyr Ala Gly His Val Thr Gly His Arg	574
180 185 190	

(2) INFORMATION FOR SEQ ID NO: 119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala	
1 5 10 15	
Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val	
20 25 30	
Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe	
35 40 45	
Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Thr Ser	

181

50

55

60

Ala Val Asn Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile Thr Asn Asp
 65 70 75 80

Cys Pro Asn Ser Ser Ile Val Tyr Glu Thr Glu His His Ile Leu His
 85 90 95

Leu Pro Gly Cys Leu Pro Cys Val Arg Val Gly Asn Gln Ser Arg Cys
 100 105 110

Trp Val Ala Leu Thr Pro Thr Val Ala Ala Pro Tyr Ile Gly Ala Pro
 115 120 125

Leu Glu Ser Leu Arg Ser His Val Asp Leu Met Val Gly Ala Ala Thr
 130 135 140

Ala Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu
 145 150 155 160

Val Gly Gln Met Phe Ser Phe Gln Pro Arg Arg His Trp Thr Thr Gln
 165 170 175

Asp Cys Asn Cys Ser Ile Tyr Ala Gly His Val Thr Gly His Arg
 180 185 190

(2) INFORMATION FOR SEQ ID NO: 120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 574 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: GB549-4-3

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..574

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

ACG TGC GGC TTT GCC GAC CTC ATG GGA TAC ATC CCG CTC GTG GGC GCC
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala
 1 5 10 15

48

CCT GTG GGT GGC GTC GCC AGG GCC TTG GCA CAT GGT GTC AGG GCC GTG
 Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val
 20 25 30

96

GAG GAC GGG ATT AAC TAT GCA ACA GGG AAT CTT CCC GGT TGC TCC TTT Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe 35 40 45	144
TCT ATC TTC CTT CTA GCA CTT CTC TCG TGC TTG ACT GTC CCG GCC TCG Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser 50 55 60	192
GCG CAG CAC TAC CGG AAC ATC TCG GGC ATT TAT CAC GTC ACC AAT GAC Ala Gln His Tyr Arg Asn Ile Ser Gly Ile Tyr His Val Thr Asn Asp 65 70 75 80	240
TGC CCG AAC TCT AGT ATA GTG TAT GAA GCT GAC CAT CAT ATC ATG CAT Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Met His 85 90 95	288
CTA CCA GGG TGT GTG CCT TGC GTG AGA ACC GGG AAC ACC TCG CGC TGC Leu Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Thr Ser Arg Cys 100 105 110	336
TGG GTT CCT TTA ACA CCC ACT GTG GCT GCC CCC TAT GTT GGC GCG CCG Trp Val Pro Leu Thr Pro Thr Val Ala Ala Pro Tyr Val Gly Ala Pro 115 120 125	384
CTC GAA TCC ATG CGG CGG CAC GTG GAC TTA ATG GTG GGT GCC GCC ACC Leu Glu Ser Met Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr 130 135 140	432
GTC TGC TCG GCC CTG TAC ATC GGA GAC CTT TGC GGA GGT GTC TTC CTG Val Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Val Phe Leu 145 150 155 160	480
GTC GGG CAG ATG TTC ACC TTC CGG CGC CGC CAT TGG ACT ACC CAG Val Gly Gln Met Phe Thr Phe Arg Pro Arg Arg His Trp Thr Thr Gln 165 170 175	528
GAC TGC AAC TGC TCT ATC TAT GAT GGC CAC ATC ACC GGC CAT AGA A Asp Cys Asn Cys Ser Ile Tyr Asp Gly His Ile Thr Gly His Arg 180 185 190	574

(2) INFORMATION FOR SEQ ID NO: 121:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 191 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala 1 5 10 15
Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val 20 25 30

Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe
 35 40 45

Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser
 50 55 60

Ala Gln His Tyr Arg Asn Ile Ser Gly Ile Tyr His Val Thr Asn Asp
 65 70 75 80

Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Met His
 85 90 95

Leu Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Thr Ser Arg Cys
 100 105 110

Trp Val Pro Leu Thr Pro Thr Val Ala Ala Pro Tyr Val Gly Ala Pro
 115 120 125

Leu Glu Ser Met Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr
 130 135 140

Val Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu
 145 150 155 160

Val Gly Gln Met Phe Thr Phe Arg Pro Arg Arg His Trp Thr Thr Gln
 165 170 175

Asp Cys Asn Cys Ser Ile Tyr Asp Gly His Ile Thr Gly His Arg
 180 185 190

(2) INFORMATION FOR SEQ ID NO: 122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 574 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: GB809-4-3

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..574

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

ACG TGC GGC TTC GCC GAC CTC ATG GGA TAC ATC CCG CTC GTG GGC GCC

48

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala 1 5 10 15			
CCC GTT GGG GGC GTC GCC AGG GCC CTG GCG CAT GGC GTC AGG GCT GTG Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val 20 25 30			96
GAG GAC GGG ATT AAC TAT GCG ACA GGG AAT CTT CCC GGT TGC TCT TTC Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe 35 40 45			144
TCT ATC TTC CTC CTG GCA CTT TCG TGC CTC ACT GTC CCA GCG TCA Ser Ile Phe Leu Leu Ala Leu Ser Cys Leu Thr Val Pro Ala Ser 50 55 60			192
GCT GAG CAC TAC CGG AAT GCT TCG GGC ATC TAT CAC ATC ACC AAT GAC Ala Glu His Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile Thr Asn Asp 65 70 75 80			240
TGT CCG AAT TCC AGC GTA GTC TAT GAA ACT GAC CAC CAT ATA TTG CAC Cys Pro Asn Ser Ser Val Val Tyr Glu Thr Asp His His Ile Leu His 85 90 95			288
TTG CCG GGG TGC GTA CCC TGC GTG AGG GCC GGG AAC GTG TCT CGT TGC Leu Pro Gly Cys Val Pro Cys Val Arg Ala Gly Asn Val Ser Arg Cys 100 105 110			336
TGG ACG CCG GTA ACA CCT ACG GTG GCT GCC GTA TCC ATG GAC GCT CCG Trp Thr Pro Val Thr Pro Thr Val Ala Ala Val Ser Met Asp Ala Pro 115 120 125			384
CTC GAG TCC TTC CGG CGG CAT GTG GAC CTA ATG GTA GGT GCG GCC ACC Leu Glu Ser Phe Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr 130 135 140			432
GTG TGT TCT GTC CTC TAT GTT GGA GAC CTC TGT GGA GGT GCT TTC CTA Val Cys Ser Val Leu Tyr Val Gly Asp Leu Cys Gly Gly Ala Phe Leu 145 150 155 160			480
GTG GGG CAG ATG TTC ACC TTC CAG CCG CGT CGC CAC TGG ACC ACG CAG Val Gly Gln Met Phe Thr Phe Gln Pro Arg Arg His Trp Thr Gln 163 170 175			528
GAT TGT AAT TGC TCC ATC TAT ACT GGC CAT ATC ACC GGC CAC AGG A Asp Cys Asn Cys Ser Ile Tyr Thr Gly His Ile Thr Gly His Arg 180 185 190			574

(2) INFORMATION FOR SEQ ID NO: 123:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 191 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala
1 5 10 15

Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val
20 25 30

Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe
35 40 45

Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser
50 55 60

Ala Glu His Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile Thr Asn Asp
65 70 75 80

Cys Pro Asn Ser Ser Val Val Tyr Glu Thr Asp His His Ile Leu His
85 90 95

Leu Pro Gly Cys Val Pro Cys Val Arg Ala Gly Asn Val Ser Arg Cys
100 105 110

Trp Thr Pro Val Thr Pro Thr Val Ala Ala Val Ser Met Asp Ala Pro
115 120 125

Leu Glu Ser Phe Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr
130 135 140

Val Cys Ser Val Leu Tyr Val Gly Asp Leu Cys Gly Gly Ala Phe Leu
145 150 155 160

Val Gly Gln Met Phe Thr Phe Gln Pro Arg Arg His Trp Thr Thr Gln
165 170 175

Asp Cys Asn Cys Ser Ile Tyr Thr Gly His Ile Thr Gly His Arg
180 185 190

(2) INFORMATION FOR SEQ ID NO: 124:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..31
- (D) OTHER INFORMATION: /standard_name= "HCV Primer HCPr206"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

TGGGGATCCC GTATGATACC CGCTGCTTG A

(2) INFORMATION FOR SEQ ID NO: 125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..30
- (D) OTHER INFORMATION: /standard_name= "HCV Primer HcPr207"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

GGCGGAATTC CTGGTCATAG CCTCCGTGAA

(2) INFORMATION FOR SEQ ID NO: 126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: amino acid
- (C) INDIVIDUAL ISOLATE: GB358

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

Val	Asn	Tyr	Arg	Asn	Ala	Ser	Gly	Ile	Tyr	His	Ile
1					5				10		

(2) INFORMATION FOR SEQ ID NO: 127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Amino acid
- (C) INDIVIDUAL ISOLATE: GB549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

Gln His Tyr Arg Asn Ile Ser Gly Ile Tyr His Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Amino acid
- (C) INDIVIDUAL ISOLATE: GB809

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

Glu His Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile
1 5 10

(2) INFORMATION FOR SEQ ID NO: 129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: amino acid
- (C) INDIVIDUAL ISOLATE: GB358

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

Val Tyr Glu Thr Glu His His Ile Leu His Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 130:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: amino acid
(C) INDIVIDUAL ISOLATE: GB549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

Val Tyr Glu Ala Asp His His Ile Met His Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 131:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: amino acid
(C) INDIVIDUAL ISOLATE: GB809

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

Val Tyr Glu Thr Asp His His Ile Leu His Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 132:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: amino acid
(C) INDIVIDUAL ISOLATE: GB358

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

Val Arg Val Gly Asn Gln Ser Arg Cys Trp Val Ala Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: amino acid
- (C) INDIVIDUAL ISOLATE: GB549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

Val Arg Thr Gly Asn Thr Ser Arg Cys Trp Val Pro Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: amino acid
- (C) INDIVIDUAL ISOLATE: GB809

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

Val Arg Ala Gly Asn Val Ser Arg Cys Trp Thr Pro Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: amino acid

(C) INDIVIDUAL ISOLATE: GB358

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

Ala Pro Tyr Ile Gly Ala Pro Leu Glu Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO: 136:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: amino acid

(C) INDIVIDUAL ISOLATE: GB3549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

Ala Pro Tyr Val Gly Ala Pro Leu Glu Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO: 137:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: amino acid

(C) INDIVIDUAL ISOLATE: GB809

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

Ala Val Ser Met Asp Ala Pro Leu Glu Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO: 138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: amino acid
- (C) INDIVIDUAL ISOLATE: GB358 and GB809

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:

Gln	Pro	Arg	Arg	His	Trp	Thr	Thr	Gln	Asp
1				5				10	

(2) INFORMATION FOR SEQ ID NO: 139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: amino acid
- (C) INDIVIDUAL ISOLATE: GB549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

Arg	Pro	Arg	Arg	His	Trp	Thr	Thr	Gln	Asp
1				5				10	

(2) INFORMATION FOR SEQ ID NO: 140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

SUBSTITUTE SHEET (RULE 26)

- (A) ORGANISM: amino acid
- (C) INDIVIDUAL ISOLATE: GB549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

Arg Pro Arg Arg His Trp Thr Thr Gln Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO: 141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

TGGGATATGA TGATGAACTG GTC

23

(2) INFORMATION FOR SEQ ID NO: 142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

CCAGGTACAA CGGAACCAAT TGCC

24

(2) INFORMATION FOR SEQ ID NO: 143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 957 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..957

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 1..954

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

ATG AGC ACA AAT CCT AAA CCT CAA AGA AAA ACC AAA AGA AAC ACT AAC	48
Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn	
1 5 10 15	
CGC CGC CCA CAG GAC GTC AAG TTC CCG GGC GGT GGC CAG ATC GTT GGT	96
Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly	
20 25 30	
GGA GTA TAC TTG TTG CCG CGC AGG GGC CCC CGG TTG GGT GTG CGC GCG	144
Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala	
35 40 45	
ACG AGG AAA ACT TCC GAG CGG TCC CAG CCA CGT GGG AGG CGC CAG CCC	192
Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro	
50 55 60	
ATC CCC AAA GAT CGG CGC CCC ACT GGC AAG TCC TGG GGA AAA CCA GGA	240
Ile Pro Lys Asp Arg Arg Pro Thr Gly Lys Ser Trp Gly Lys Pro Gly	
65 70 75 80	
TAC CCT TGG CCC CTG TAC GGG AAT GAG GGC CTC GGC TGG GCA GGG TGG	288
Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Leu Gly Trp Ala Gly Trp	
85 90 95	
CTC CTG TCC CCC CGA GGG TCT CGC CCG TCA TGG GGC CCA ACT GAC CCC	336
Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro	
100 105 110	
CGG CAC AGG TCA CGC AAC TTG GGT AAG GTC ATC GAT ACC CTT ACG TGT	384
Arg His Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys	
115 120 125	
GGC TTT GCC GAC CTC ATG GGG TAC ATC CCT GTC GTC GGC GCC CCA GTT	432
Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Val Val Gly Ala Pro Val	
130 135 140	
GGT GGT GTC GCC AGA GCT CTC GCG CAT GGC GTG AGA GTT CTG GAA GAC	480
Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp	
145 150 155 160	

GGG ATA AAC TAT GCA ACA GGG AAC TTG CCC GGT TGC TCC TTT TCT ATC Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile 165 170 175	528
TTC TTA TTG GCC CTG CTA TCT TGT ATC ACT GTG CCG GTC TCC GGC TTG Phe Leu Leu Ala Leu Leu Ser Cys Ile Thr Val Pro Val Ser Gly Leu 180 185 190	576
CAG GTC AAG AAC ACC AGC AGC TCT TAC ATG GTA ACC AAT GAC TGC CAG Gln Val Lys Asn Thr Ser Ser Tyr Met Val Thr Asn Asp Cys Gln 195 200 205	624
AAC AGT AGC ATC GTC TGG CAG CTC AGG GAT GCT GTT CTT CAC GTC CCC Asn Ser Ser Ile Val Trp Gln Leu Arg Asp Ala Val Leu His Val Pro 210 215 220	672
GGG TGT GTC CCT TGT GAG GAG AAG GGC AAC ATA TCC CGC TGT TGG ATA Gly Cys Val Pro Cys Glu Glu Lys Gly Asn Ile Ser Arg Cys Trp Ile 225 230 235 240	720
CCG GTT TCG CCC AAT ATA GCT GTG AGC CAA CCT GGT GCG CTT ACC AAG Pro Val Ser Pro Asn Ile Ala Val Ser Gln Pro Gly Ala Leu Thr Lys 245 250 255	768
GGC CTG CGG ACG CAT ATT GAT ACC ATC ATT GCA TCC GCT ACG TTT TGC Gly Leu Arg Thr His Ile Asp Thr Ile Ile Ala Ser Ala Thr Phe Cys 260 265 270	816
TCT GCC CTG TAC ATA GGA GAC CTG TGT GGC GCG GTG ATG TTG GCT TCT Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Ala Val Met Leu Ala Ser 275 280 285	864
CAA GTC TTC ATC ATC TCG CCC CRG CAT CAT AAG TTT GTC CAG GAC TGC Gln Val Phe Ile Ile Ser Pro Gln His His Lys Phe Val Gln Asp Cys 290 295 300	912
AAC TGT TCC ATA TAC CCA GGC CAC ATC ACT GGA CAT CGG ATG GCG Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg Met Ala 305 310 315	957

(2) INFORMATION FOR SEQ ID NO: 144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(iii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn 1 5 10 15
Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gln Ile Val Gly 20 25 30

Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala
 35 40 45

Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro
 50 55 60

Ile Pro Lys Asp Arg Arg Pro Thr Gly Lys Ser Trp Gly Lys Pro Gly
 65 70 75 80

Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Leu Gly Trp Ala Gly Trp
 85 90 95

Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
 100 105 110

Arg His Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys
 115 120 125

Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Val Val Gly Ala Pro Val
 130 135 140

Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp
 145 150 155 160

Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile
 165 170 175

Phe Leu Leu Ala Leu Leu Ser Cys Ile Thr Val Pro Val Ser Gly Leu
 180 185 190

Gln Val Lys Asn Thr Ser Ser Tyr Met Val Thr Asn Asp Cys Gln
 195 200 205

Asn Ser Ser Ile Val Trp Gln Leu Arg Asp Ala Val Leu His Val Pro
 210 215 220

Gly Cys Val Pro Cys Glu Glu Lys Gly Asn Ile Ser Arg Cys Trp Ile
 225 230 235 240

Pro Val Ser Pro Asn Ile Ala Val Ser Gln Pro Gly Ala Leu Thr Lys
 245 250 255

Gly Leu Arg Thr His Ile Asp Thr Ile Ile Ala Ser Ala Thr Phe Cys
 260 265 270

Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Ala Val Met Leu Ala Ser
 275 280 285

Gln Val Phe Ile Ile Ser Pro Gln His His Lys Phe Val Gln Asp Cys
 290 295 300

Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg Met Ala
 305 310 315

(2) INFORMATION FOR SEQ ID NO: 1:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 340 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 2..337

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:

C TCA ACG GTC ACG GAG AGG GAC ATC AGA ACT GAG GAG TCC ATA TAC Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Glu Ser Ile Tyr 1 5 10 15	46
CTT GCT TGC TCT TTA CCC GAG CAG GCA CGG ACT GCC ATA CAC TCA CTG Leu Ala Cys Ser Leu Pro Glu Gln Ala Arg Thr Ala Ile His Ser Leu 20 25 30	94
ACT GAG AGG CTT TAC GTG GGA GGG CCC ATG CTR AAC AGC AAA GGG CAA Thr Glu Arg Leu Tyr Val Gly Gly Pro Met Leu Asn Ser Lys Gly Gln 35 40 45	142
ACC TGC GGA TAC AGA CGC TGC CGC GCC AGC GGA GTG TTC ACC ACT AGC Thr Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser 50 55 60	190
ATG GGA AAT ACC ATC ACG TGC TAC GTG AAG GCA CAA GCA GCC TGT AAG Met Gly Asn Thr Ile Thr Cys Tyr Val Lys Ala Gln Ala Ala Cys Lys 65 70 75	238
GCT GCG GGC ATA ATT GCC CCC ACG ATG CTG GTG TGC GGC GAC GAT CTA Ala Ala Gly Ile Ile Ala Pro Thr Met Leu Val Cys Gly Asp Asp Leu 80 85 90 95	286
GTT GTC ATC TCA GAG AGT CAG GGG ACC GAG GAG GAC GAG CGG AAC CTA Val Val Ile Ser Glu Ser Gln Gly Thr Glu Glu Asp Glu Arg Asn Leu 100 105 110	334
CGA GCC Arg Ala	340

(2) INFORMATION FOR SEQ ID NO: 146:

(i) SEQUENCE CHARACTERISTICS:

SUBSTITUTE SHEET (RULE 26)

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:

Ser	Thr	Val	Thr	Glu	Arg	Asp	Ile	Arg	Thr	Glu	Glu	Ser	Ile	Tyr	Leu
1															
														10	15
Ala	Cys	Ser	Leu	Pro	Glu	Gln	Ala	Arg	Thr	Ala	Ile	His	Ser	Leu	Thr
														20	25
Glu	Arg	Leu	Tyr	Val	Gly	Gly	Pro	Met	Leu	Asn	Ser	Lys	Gly	Gln	Thr
														35	40
Cys	Gly	Tyr	Arg	Arg	Cys	Arg	Ala	Ser	Gly	Val	Phe	Thr	Thr	Ser	Met
														50	55
Gly	Asn	Thr	Ile	Thr	Cys	Tyr	Val	Lys	Ala	Gln	Ala	Ala	Cys	Lys	Ala
														65	70
Ala	Gly	Ile	Ile	Ala	Pro	Thr	Met	Leu	Val	Cys	Gly	Asp	Asp	Leu	Val
														85	90
Val	Ile	Ser	Glu	Ser	Gln	Gly	Thr	Glu	Glu	Asp	Glu	Arg	Asn	Leu	Arg
														100	105
															110

Ala

(2) INFORMATION FOR SEQ ID NO: 147:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 345 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..345

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..342

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

ATG AGC ACA CTT CCT AAA CCA CAA AGA AAA ACC AAA AGA AAC ACC AAC

C T

Met Ser Thr Leu Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn				
1	5	10	15	
CCC GGC CAC AGG ACG TTA AGT TCC CAG GCG GCG GTC AGA TCG TTG GTG				96
Pro Gly His Arg Thr Leu Ser Ser Gln Ala Ala Val Arg Ser Leu Val				
20	25	30		
GAG TTT ACG TGC TAC CAC GCA GGG GCC CCC AGT TGG GTG TGC GTG CAG				144
Glu Phe Thr Cys Tyr His Ala Gly Ala Pro Ser Trp Val Cys Val Gln				
35	40	45		
TGC GCA AGA CTT CCG AGC GGT CGC AAC CTC GCA GTA GCC GGC AAC CCA				192
Cys Ala Arg Leu Pro Ser Gly Arg Asn Leu Ala Val Gly Ala Asn Pro				
50	55	60		
TCC CCA GGG CGC GCC GAA CCG AGG GCA GGT CCT GGG CTC AGC CCG GGT				240
Ser Pro Gly Arg Ala Glu Pro Arg Ala Gly Pro Gly Leu Ser Pro Gly				
65	70	75	80	
ACC CTT GGC CCC TAT ATG GGA ATG AGG GCT GCG GGT GGG CAG GGT GGC				288
Thr Leu Gly Pro Tyr Met Gly Met Arg Ala Ala Gly Gln Gly Gly				
85	90	95		
TCC TGT CCC CGC GCG GCT CTC GCC CGT CGT GGG GCC CAA ATG ACC CCC				336
Ser Cys Pro Arg Ala Ala Leu Ala Arg Arg Gly Ala Gln Met Thr Pro				
100	105	110		
GGC GCA GGA				345
Gly Ala Gly				
115				

(2) INFORMATION FOR SEQ ID NO: 148:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 115 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:

Met Ser Thr Leu Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn				
1	5	10	15	
Pro Gly His Arg Thr Leu Ser Ser Gln Ala Ala Val Arg Ser Leu Val				
20	25	30		
Glu Phe Thr Cys Tyr His Ala Gly Ala Pro Ser Trp Val Cys Val Gln				
35	40	45		
Cys Ala Arg Leu Pro Ser Gly Arg Asn Leu Ala Val Gly Ala Asn Pro				
50	55	60		
Ser Pro Gly Arg Ala Glu Pro Arg Ala Gly Pro Gly Leu Ser Pro Gly				
65	70	75	80	
Thr Leu Gly Pro Tyr Met Gly Met Arg Ala Ala Gly Gln Gly Gly				

85

90

95

Ser Cys Pro Arg Ala Ala Leu Ala Arg Arg Gly Ala Gln Met Thr Pro
 100 105 110

Gly Ala Gly
 115

(2) INFORMATION FOR SEQ ID NO: 149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..280

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 2..277

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

G GCC TGT GAC CTC AAG GAC GAG GCT AGG AGG GTG ATA ACT TCA CTC
 Ala Cys Asp Leu Lys Asp Glu Ala Arg Arg Val Ile Thr Ser Leu
 1 5 10 15

46

ACG GAG CGG CTT TAC TGT GGT CCT ATG TTC AAC AGC AAG GGA CAA
 Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly Gln
 20 25 30

94

CAC TGC GGT TAC CGC CGC TGC CGT GCT AGT GGG GTG CTA CCC ACC AGC
 His Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr Ser
 35 40 45

142

TTC GGG AAC ACA ATC ACC TGT TAC ATC AAA GCA AAG GCA GCT ACC AAA
 Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Lys Ala Ala Thr Lys
 50 55 60

190

GCT GCC GGA ATT AAA AAT CCA TCA TTC CTT GTC TGC GGA GAT GAC TTG
 Ala Ala Gly Ile Lys Asn Pro Ser Phe Leu Val Cys Gly Asp Asp Leu
 65 70 75

238

GTC GTG ATT GCT GAG AGT GCA GGG ATC GAT GAG GAC AGA GCG
 Val Val Ile Ala Glu Ser Ala Gly Ile Asp Glu Asp Arg Ala
 80 85 90

280

(2) INFORMATION FOR SEQ ID NO: 150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids

(B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:

Ala Cys Asp Leu Lys Asp Glu Ala Arg Arg Val Ile Thr Ser Leu Thr
 1 5 10 15

Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly Gln His
 20 25 30

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr Ser Phe
 35 40 45

Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Lys Ala Ala Thr Lys Ala
 50 55 60

Ala Gly Ile Lys Asn Pro Ser Phe Leu Val Cys Gly Asp Asp Leu Val
 65 70 75 80

Val Ile Ala Glu Ser Ala Gly Ile Asp Glu Asp Arg Ala
 85 90

(2) INFORMATION FOR SEQ ID NO: 151:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 499 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 1..499

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
 (B) LOCATION: 1..496

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA AGA AAC ACC AAC
 Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn
 1 5 10 15

48

CGT CGC CCA CAG GAC GTC AAG TTC CCG GGC GGT GGT CAG ATC GTT GGC
 Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gln Ile Val Gly
 20 25 30

96

GGA GTT TAC TTG TTG CCG CGC AGG GGC CCT AGG ATG GGT GTG CGC GCG Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Met Gly Val Arg Ala 35 40 45	144
ACT CGG AAG ACT TCG GAA CGG TCG CAA CCC CGT GGA CGG CGT CAG CCT Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro 50 55 60	192
ATT CCC AAG GCG CGC CAG CCC ACG GGC CGG TCC TGG GGT CAA CCC GGG Ile Pro Lys Ala Arg Gln Pro Thr Gly Arg Ser Trp Gly Gln Pro Gly 65 70 75 80	240
TAC CCT TGG CCC CTT TAC GCC AAT GAG GGC CTC GGG TGG GCA GGG TGG Tyr Pro Trp Pro Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly Trp 85 90 95	288
CTG CTC TCC CCT CGA GGC TCT CGG CCT AAT TGG GGC CCC AAT GAC CCC Leu Leu Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp Pro 100 105 110	336
CGG CGA AAA TCG CGT AAT TTG GGT AAG GTC ATC GAT ACC CTA ACG TGC Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys 115 120 125	384
GGA TTC GCC GAT CTC ATG GGG TAT ATC CCG CTC GTA GGC GGC CCC ATT Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly Pro Ile 130 135 140	432
GGG GGC GTC GCA AGG GCT CTC GCA CAC GGT GTG AGG GTC CTT GAG GAC Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp 145 150 155 160	480
GGG GTA AAC TAT GCA ACA G Gly Val Asn Tyr Ala Thr 165	499

(2) INFORMATION FOR SEQ ID NO: 152:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 166 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn 1 5 10 15
Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gln Ile Val Gly 20 25 30
Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Met Gly Val Arg Ala 35 40 45

Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro
50 55 60

Ile Pro Lys Ala Arg Gln Pro Thr Gly Arg Ser Trp Gly Gln Pro Gly
65 70 75 80

Tyr Pro Trp Pro Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly Trp
85 90 95

Leu Leu Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp Pro
100 105 110

Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys
115 120 125

Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly Pro Ile
130 135 140

Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp
145 150 155 160

Gly Val Asn Tyr Ala Thr
165

(2) INFORMATION FOR SEQ ID NO: 153:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 579 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..579

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

ACG TGC GGA TTC GCC GAT CTC ATG GGG TAC ATC CCG CTC GTA GGC GGC
Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly
1 5 10 15

48

CCC GTT GGG GGC GTC GCA AGG GCT CTC GCA CAC GGT GTG AGG GTC CTT
Pro Val Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu
20 25 30

96

GAG GAC GGG GTA AAC TAT CCA ACA GGG AAT TTA CCC GGT TGC TCT TTC

144

Glu Asp Gly Val Asn Tyr Pro Thr Gly Asn Leu Pro Gly Cys Ser Phe			
35	40	45	
TCT ATC TTT ATT CTT GCT CTT CTC TCG TGT CTG ACC GTT CCG GCC TCT		192	
Ser Ile Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser			
50	55	60	
GCA GTT CCC TAC CGA AAT GCC TCT GGG ATT TAT CAT GTT ACC AAT GAT		240	
Ala Val Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp			
65	70	75	80
TGC CCA AAC TCT TCC ATA GTC TAT GAG GCA GAT AAC CTG ATC CTA CAC		288	
Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asn Leu Ile Leu His			
85	90	95	
GCA CCT GGT TGC GTG CCT TGT GTC ATG ACA GGT AAT GTG AGT AGA TGC		336	
Ala Pro Gly Cys Val Pro Cys Val Met Thr Gly Asn Val Ser Arg Cys			
100	105	110	
TGG GTC CAA ATT ACC CCT ACA CTG TCA GCC CCG AGC CTC GGA GCA GTC		384	
Trp Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Leu Gly Ala Val			
115	120	125	
ACG GCT CCT CTT CGG AGA GCC GTT GAC TAC CTA GCG GGA GGG GCT GCC		432	
Thr Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala Gly Gly Ala Ala			
130	135	140	
CTC TGC TCC GCG TTA TAC GTA GGA GAC GCG TGT GGG GCA CTA TTC TTG		480	
Leu Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe Leu			
145	150	155	160
GTA GGC CAA ATG TTC ACC TAT AGG CCT CGC CAG CAC GCT ACG GTG CAG		528	
Val Gly Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val Gln			
165	170	175	
AAC TGC AAC TGT TCC ATT TAC AGT GGC CAT GTT ACC GGC CAC CGG ATG		576	
Asn Cys Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Arg Met			
180	185	190	
GGC		579	
Ala			

(2) INFORMATION FOR SEQ ID NO: 154:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly
 1 5 10 15

Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu
20 25 30

Glu Asp Gly Val Asn Tyr Pro Thr Gly Asn Leu Pro Gly Cys Ser Phe
35 40 45

Ser Ile Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser
50 55 60

Ala Val Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp
65 70 75 80

Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asn Leu Ile Leu His
85 90 95

Ala Pro Gly Cys Val Pro Cys Val Met Thr Gly Asn Val Ser Arg Cys
100 105 110

Trp Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Leu Gly Ala Val
115 120 125

Thr Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala Gly Gly Ala Ala
130 135 140

Leu Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe Leu
145 150 155 160

Val Gly Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val Gln
165 170 175

Asn Cys Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Arg Met
180 185 190

Ala

(2) INFORMATION FOR SEQ ID NO: 155:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 579 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 1..579

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
(B) LOCATION: 1..576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

ACG TGC GGA TTC GCC GAC CTC GTG GGG TAC ATC CCG CTC GTA GGC GGC	48
Thr Cys Gly Phe Ala Asp Leu Val Gly Tyr Ile Pro Leu Val Gly Gly	
1 5 10 15	
CCC GTT GGG GGC GTC GCA AGG GCT CTC GCA CAT GGT GTG AGG GTT CTT	96
Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu	
20 25 30	
GAG GAC GGG GTG AAT TAT GCA ACA GGG AAT CTG CCT GGT TGC TCT TTC	144
Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe	
35 40 45	
TCT ATC TTC ATT CTT GCA CTT CTC TCG TGC CTC ACT GTC CCG GCC TCT	192
Ser Ile Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser	
50 55 60	
GCA GTT CCC TAC CGA AAT GCC TCT GGG ATC TAT CAT GTC ACC AAT GAT	240
Ala Val Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp	
65 70 75 80	
TGC CCA AAC TCT TCC ATA GTC TAT GAG GCA GAT GAT CTG ATC CTA CAC	288
Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Leu Ile Leu His	
85 90 95	
GCA CCT GGC TGC GTG CCT TGT GTC AGG AAA GAT AAT GTG AGT AGG TGC	336
Ala Pro Gly Cys Val Pro Cys Val Arg Lys Asp Asn Val Ser Arg Cys	
100 105 110	
TGG GTC CAA ATT ACC CCC ACG CTG TCA GCC CCG AGC TTC GGA GCA GTC	384
Trp Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Phe Gly Ala Val	
115 120 125	
ACG GCT CCC CTT CGG AGA GCC GTT GAT TAC TTG GTG GGA GGG GCT GCC	432
Thr Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Val Gly Gly Ala Ala	
130 135 140	
CTC TGC TCC GCG TTA TAC GTT GGA GAC GCG TGT GGG GCA CTA TTT TTG	480
Leu Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe Leu	
145 150 155 160	
GTA GGC CAA ATG TTC ACC TAT AGG CCT CGC CAG CAT GCT ACG GTG CAG	528
Val Gly Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val Gln	
165 170 175	
GAC TGC AAC TGT TCC ATC TAC AGT GGC CAC GTC ACC GGC CAT CAG ATG	576
Asp Cys Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Gln Met	
180 185 190	
GCA	579
Ala	

(2) INFORMATION FOR SEQ ID NO: 156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

Thr Cys Gly Phe Ala Asp Leu Val Gly Tyr Ile Pro Leu Val Gly Gly
1 5 10 15

Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu
20 25 30

Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe
35 40 45

Ser Ile Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser
50 55 60

Ala Val Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp
65 70 75 80

Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Leu Ile Leu His
85 90 95

Ala Pro Gly Cys Val Pro Cys Val Arg Lys Asp Asn Val Ser Arg Cys
100 105 110

Trp Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Phe Gly Ala Val
115 120 125

Thr Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Val Gly Gly Ala Ala
130 135 140

Leu Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe Leu
145 150 155 160

Val Gly Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val Gln
165 170 175

Asp Cys Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Gln Met
180 185 190

Ala

(2) INFORMATION FOR SEQ ID NO: 157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 530 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 3..530

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 3..527

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

CA CCT ACG ACA GCT CTG CTG GTG GCC CAG TTA CTG CGG ATT CCC CAA Pro Thr Thr Ala Leu Leu Val Ala Gln Leu Leu Arg Ile Pro Gln	1	5	10	15	47
GTC GTC ATT GAC ATC ATC GCA GGG AGC CAC TGG GGG GTC TTG TTT GGC Val Val Ile Asp Ile Ile Ala Gly Ser His Trp Gly Val Leu Phe Ala	20		25		95
GCC GCA TAC TAT GCA TCG GTG GCT AAC TGG ACC AAG GTC GTG CTG GTC Ala Ala Tyr Tyr Ala Ser Val Ala Asn Trp Thr Lys Val Val Leu Val	35		40		143
TTG TTT CTG TTT GCA GGG GTT GAT GCT ACT ACC CAG ATT TCG GGC GGC Leu Phe Leu Phe Ala Gly Val Asp Ala Thr Thr Gln Ile Ser Gly Gly	50		55		191
TCC AGC GCC CAA ACG ACG TAT GGC ATC GCC TCA TTT ATC ACC ACC CGC GGC Ser Ser Ala Gln Thr Thr Tyr Gly Ile Ala Ser Phe Ile Thr Arg Gly	65		70		239
GCG CAG CAG AAA CTG CAG CTC ATA AAT ACC AAC GGA AGC TGG CAC ATC Ala Gln Gln Lys Leu Gln Leu Ile Asn Thr Asn Gly Ser Trp His Ile	80		85		287
AAC AGG ACC GCC CTT AAT TGT AAT GAC AGC CTC CAG ACT GGG TTC ATA Asn Arg Thr Ala Leu Asn Cys Asn Asp Ser Leu Gln Thr Gly Phe Ile	100		105		335
GCC GGC CTC TTC TAC TAC CAT AAG TTC AAC TCT TCT GGA TGC CCG GAT Ala Gly Leu Phe Tyr Tyr His Lys Phe Asn Ser Ser Gly Cys Pro Asp	115		120		383
CGG ATG GCT AGC TGT AGG GCC CTT GCC ACT TTT GAC CAG GGC TGG GGA Arg Met Ala Ser Cys Arg Ala Leu Ala Thr Phe Asp Gln Gly Trp Gly	130		135		431
ACT ATC AGC TAT GCC AAC ATA TCG TGT CCC AGT GAT GAC AAA CCA TAT Thr Ile Ser Tyr Ala Asn Ile Ser Gly Pro Ser Asp Asp Lys Pro Tyr	145		150		479
TGC TGG CAC TAT CCC CCA CGG CCG TGC GGA GTG GTG CCA GCC CAA GAG					52

Cys Trp His Tyr Pro Pro Arg Pro Cys Gly Val Val Pro Ala Gln Glu
160 165 170 175

GTC
Val

530

(2) INFORMATION FOR SEQ ID NO: 158:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 176 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:

Pro Thr Thr Ala Leu Leu Val Ala Gln Leu Leu Arg Ile Pro Gln Val
1 5 10 15

Val Ile Asp Ile Ile Ala Gly Ser His Trp Gly Val Leu Phe Ala Ala
20 25 30

Ala Tyr Tyr Ala Ser Val Ala Asn Trp Thr Lys Val Val Leu Val Leu
35 40 45

Phe Leu Phe Ala Gly Val Asp Ala Thr Thr Gln Ile Ser Gly Gly Ser
50 55 60

Ser Ala Gln Thr Thr Tyr Gly Ile Ala Ser Phe Ile Thr Arg Gly Ala
65 70 75 80

Gln Gln Lys Leu Gln Leu Ile Asn Thr Asn Gly Ser Trp His Ile Asn
85 90 95

Arg Thr Ala Leu Asn Cys Asn Asp Ser Leu Gln Thr Gly Phe Ile Ala
100 105 110

Gly Leu Phe Tyr Tyr His Lys Phe Asn Ser Ser Gly Cys Pro Asp Arg
115 120 125

Met Ala Ser Cys Arg Ala Leu Ala Thr Phe Asp Gln Gly Trp Gly Thr
130 135 140

Ile Ser Tyr Ala Asn Ile Ser Gly Pro Ser Asp Asp Lys Pro Tyr Cys
145 150 155 160

Trp His Tyr Pro Pro Arg Pro Cys Gly Val Val Pro Ala Gln Glu Val
165 170 175

(2) INFORMATION FOR SEQ ID NO: 159:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 340 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 2..340

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 2..337

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

C TCG ACC GTT ACC GAA CAT GAC ATA ATG ACC GAA GAG TCC ATT TAC Ser Thr Val Thr Glu His Asp Ile Met Thr Glu Glu Ser Ile Tyr	46
1 5 10 15	
CAA TCA TGT GAC TTG CAG CCC GAG GCA CGC GCA GCA ATA CGG TCA CTC Gln Ser Cys Asp Leu Gln Pro Glu Ala Arg Ala Ile Arg Ser Leu	94
20 25 30	
ACC CAA CGC CTC TAC TGT GGA GGC CCC ATG TAC AAC AGC AAG GGG CAA Thr Gln Arg Leu Tyr Cys Gly Pro Met Tyr Asn Ser Lys Gly Gln	142
35 40 45	
CAG TGT GGT TAT CGC AGA TGC CGC GCC AGC GGC GTT TTC ACC ACC AGT Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser	190
50 55 60	
ATG GGC AAC ACC ATG ACG TGC TAC ATC AAG GCT TTA GCC TCC TGT AGA Met Gly Asn Thr Met Thr Cys Tyr Ile Lys Ala Leu Ala Ser Cys Arg	238
65 70 75	
GCC GCA AGG CTC CGG GAC TGC ACG CTC CTG GTG TGT GGT GAC GAT CTT Ala Ala Arg Leu Arg Asp Cys Thr Leu Leu Val Cys Gly Asp Asp Leu	286
80 85 90 95	
GTG GCC ATC TGC GAG AGC CAG GGG ACA CAC GAG GAT GAA GCA AGC CTG Val Ala Ile Cys Glu Ser Gln Gly Thr His Glu Asp Glu Ala Ser Leu	334
100 105 110	
AGA GCC Arg Ala	340

(2) INFORMATION FOR SEQ ID NO. 160:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:

Ser Thr Val Thr Glu His Asp Ile Met Thr Glu Glu Ser Ile Tyr Gln
1 5 10 15

Ser Cys Asp Leu Gln Pro Glu Ala Arg Ala Ala Ile Arg Ser Leu Thr
20 25 30

Gln Arg Leu Tyr Cys Gly Gly Pro Met Tyr Asn Ser Lys Gly Gln Gln
35 40 45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser Met
50 55 60

Gly Asn Thr Met Thr Cys Tyr Ile Lys Ala Leu Ala Ser Cys Arg Ala
65 70 75 80

Ala Arg Leu Arg Asp Cys Thr Leu Leu Val Cys Gly Asp Asp Leu Val
85 90 95

Ala Ile Cys Glu Ser Gln Gly Thr His Glu Asp Glu Ala Ser Leu Arg
100 105 110

Ala

(2) INFORMATION FOR SEQ ID NO: 161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..340

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 2..337

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

C TCA ACC GCC ACC GAA CAT GAC ATA TTG ACT GAA GAG TCC ATA TAC
Ser Thr Ala Thr Glu His Asp Ile Leu Thr Glu Glu Ser Ile Tyr

1

5

10

15

CAA TCA TGT GAC TCG CAG CCC GAC GCA CGC GCA GCA ATA CGG TCA CTC
 Gln Ser Cys Asp Ser Gln Pro Asp Ala Arg Ala Ala Ile Arg Ser Leu
 20 25 30

94

ACC CAA CGC TTG TTC TGT GGA GGC CCC ATG TAT AAC AGC AAG GGG CAA
 Thr Gln Arg Leu Phe Cys Gly Gly Pro Met Tyr Asn Ser Lys Gly Gln
 35 40 45

142

CAA TGT GGT TAT CGC AGA TGC CGC GCC AGC GGC GTC TTC ACC ACC AGT
 Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser
 50 55 60

190

ATG GGC AAC ACC ATG ACG TGC TAC ATT AAG GCT TTA GCC TCC TGT AGA
 Met Gly Asn Thr Met Thr Cys Tyr Ile Lys Ala Leu Ala Ser Cys Arg
 65 70 75

238

ACC GCT GGG CTC CGG GAC TAC ACG CTC CTG GTG TGT GGT GAC GAT CAT
 Thr Ala Gly Leu Arg Asp Tyr Thr Leu Leu Val Cys Gly Asp Asp His
 80 85 90 95

286

GTG GCC ATC TGC GAG AGC CAG GGG ACA CAC GAG GAT GAA GCG AAC CTG
 Val Ala Ile Cys Glu Ser Gln Gly Thr His Glu Asp Glu Ala Asn Leu
 100 105 110

334

AGA GCC
 Arg Ala

340

(2) INFORMATION FOR SEQ ID NO: 162:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:

Ser Thr Ala Thr Glu His Asp Ile Leu Thr Glu Glu Ser Ile Tyr Gln
 1 5 10 15

Ser Cys Asp Ser Gln Pro Asp Ala Arg Ala Ala Ile Arg Ser Leu Thr
 20 25 30
 Gln Arg Leu Phe Cys Gly Gly Pro Met Tyr Asn Ser Lys Gly Gln Gln
 35 40 45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser Met
 50 55 60

Gly Asn Thr Met Thr Cys Tyr Ile-Lys Ala Leu Ala Ser Cys Arg Thr
 65 70 75 80

Ala Gly Leu Arg Asp Tyr Thr Leu Leu Val Cys Gly Asp Asp His Val
 85 90 95

Ala Ile Cys Glu Ser Gln Gly Thr His Glu Asp Glu Ala Asn Leu Arg
 100 105 110

Ala

(2) INFORMATION FOR SEQ ID NO: 163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 499 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..499

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..496

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

ATG AGC ACG AAT CCT AAA CTT CAA AGA AAA ACC AAA CGT AAC ACC AAC	48
Met Ser Thr Asn Pro Lys Leu Gln Arg Lys Thr Lys Arg Asn Thr Asn	
1 5 10 15	
CGC CGC CCC ATG GAC GTT AAG TTC CCG GGT GGC CAG ATC GTT GGC	96
Arg Arg Pro Met Asp Val Lys Phe Pro Gly Gly Gln Ile Val Gly	
20 25 30	
GGA GTT TAC TTG TTG CCG CGC AGG GGC CCT AGG TTG GGT GTG CGC GCG	144
Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala	
35 40 45	
ACT CGG AAG ACT TCG GAG CGG TCG CAA CCT CGT GGG AGG CGC CAA CCT	192
Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro	
50 55 60	
ATC CCC AAG GCG CGC CGA TCC GAG GGC AGA TCC TGG GCG CAG CCC GGG	240
Ile Pro Lys Ala Arg Arg Ser Glu Gly Arg Ser Trp Ala Gln Pro Gly	
65 70 75 80	
TAT CCT TGG CCC CTT TAC GGC AAT GAG GGC TGT GGG TGG GCA GGG TGG	288
Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp	
85 90 95	
CTC CTG TCC CCT CGC GGG TCT CGG CCG TCT TGG GGC CCT AAT GAT CCC	336

Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro			
100	105	110	
CGG CGG AGG TCC CGC AAC CTG GGT AAG GTC ATC GAT ACC CTA ACA TGC		384	
Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys			
115	120	125	
Gly TTC GCC GAC CTC ATG GGA TAC ATC CCG CTT GTA GGC GCC CCC GTG		432	
Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala Pro Val			
130	135	140	
GCT GGC GTC GCC AGA GCC CTG GCA CAC GGT GTT AGG GCT GTG GAA GAC		480	
Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val Glu Asp			
145	150	155	160
GGG ATC AAC TAC GCA ACA G		499	
Gly Ile Asn Tyr Ala Thr			
165			

(2) INFORMATION FOR SEQ ID NO: 164:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 166 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

Met Ser Thr Asn Pro Lys Leu Gln Arg Lys Thr Lys Arg Asn Thr Asn			
1	5	10	15
Arg Arg Pro Met Asp Val Lys Phe Pro Gly Gly Gln Ile Val Gly			
20	25	30	
Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala			
35	40	45	
Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro			
50	55	60	
Ile Pro Lys Ala Arg Arg Ser Glu Gly Arg Ser Trp Ala Gln Pro Gly			
65	70	75	80
Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp			
85	90	95	
Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro			
100	105	110	
Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys			
115	120	125	
Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala Pro Val			
130	135	140	

Gly	Gly	Val	Ala	Arg	Ala	Leu	Ala	His	Gly	Val	Arg	Ala	Val	Glu	Asp
145		150						155					160		

Gly Ile Asn Tyr Ala Thr
165

(2) INFORMATION FOR SEQ ID NO: 165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 499 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

ATGAGCACGA ATCCTAACCC TCAAAGAAAA ACCAAACGTA ACACCAACCG CCGCCCTATG	60
GACGTTAAGT TCCCAGGCGG TGGTCAGATC GTTGGCGGAG TTTACTTGTT GCGCGGCAGG	120
GGCCCCAGGT TGGGTGTGCG CGCGACTCGG AAGACTTCGG AGC3GTGCA ACCTCGTGGG	180
AGGCGCCAAC CTATCCCCAA GGCGCGCCGA ACCGAGGGCA GATCCTGGG GCAGCCCCGG	240
TATCCTTGGC CCCTTTACGG CAATGAGGGC TGTGGGTGGG CAGGGTGGCT CCTGTCCCCCT	300
CGCGGNTCTC GGNCGTCTTG GGGCCCCAAT GATCCCCGGN GGAGATCCCG CAACTTGGGT	360
AAGGTCATCG ATACCCTAAC ATGCGGCTTC GCCGACCTCA TGGGATACT CATCCGTTGTA	420
GGCGCCCCCG TGGGTGGCGT CGCCAGGGCC CTGGCACATG GTGTTAGGGC TGTGGAAGAC	480
GGGATCAATT ATGCAACAG	499

(2) INFORMATION FOR SEQ ID NO: 166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn

1	5	10	15
Arg Arg Pro Met Asp Val Lys Phe Pro Gly Gly Gln Ile Val Gly			
20	25	30	
Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala			
35	40	45	
Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro			
50	55	60	
Ile Pro Lys Ala Arg Arg Thr Glu Gly Arg Ser Trp Ala Gln Pro Gly			
65	70	75	80
Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp			
85	90	95	
Leu Leu Ser Pro Arg Xaa Ser Arg Xaa Ser Trp Gly Pro Asn Asp Pro			
100	105	110	
Arg Xaa Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu			
115	120	125	

(2) INFORMATION FOR SEQ ID NO: 167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..579

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..579

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

ACA TGC GGC TTC GCC GAC CTC ATG GGA TAC ATC CCG CTT GTA GGC GCC	48
Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala	
1 5 10 15	
CCC GTG GGT GGC GTC AGG GCC-CTG GCA CAT GGT GTT AGG GCT GTG	96
Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val	
20 25 30	
GAA GAC GGG ATC AAT TAT GCA ACA GGG AAC CTT CCC GGT TGC TCC TTT	144

Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe		
35	40	45
TCT ATC TTC CTC TTG GCG CTC CTC TCG ACT GTT CCC ACA TCG		192
Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Thr Ser		
50	55	60
GCC GTT AAC TAT CGC AAT GCT TCG GGC ATT TAT CAC ATC ACC AAT GAC		240
Ala Val Asn Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile Thr Asn Asp		
65	70	75
TGC CCG AAT GCA AGC ATA GTG TAC GAG ACC GAA AAT CAC ATC TTA CAC		288
Cys Pro Asn Ala Ser Ile Val Tyr Glu Thr Glu Asn His Ile Leu His		
85	90	95
CTC CCA GGG TGC GTA CCC TGT GTG AGG ACT GGG AAC CAG TCG CGG TGT		336
Leu Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Gln Ser Arg Cys		
100	105	110
TGG GTG GCC CTC ACT CCC ACA GTA GCG TCG CCA TAC GCC GGT GCT CCG		384
Trp Val Ala Leu Thr Pro Val Ala Ser Pro Tyr Ala Gly Ala Pro		
115	120	125
CTT GAG CCC TTG CGG CGT CAT GTG GAC CTG ATG GTA GGT GCT GCC ACC		432
Leu Glu Pro Leu Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr		
130	135	140
ATG TGT TCC GCC CTC TAC ATC GGC GAC TTG TGC GGT GGC TTA TTC TTG		480
Met Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Leu Phe Leu		
145	150	155
GTG GGC CAA ATG TTC ACC TTC CAA CCG CGA CGT CAC TGG ACC ACT CAG		528
Val Gly Gln Met Phe Thr Phe Gln Pro Arg Arg His Trp Thr Thr Gln		
165	170	175
GAC TGC AAT TGT TCC ATC TAC ACG GGC CAC ATT ACG GGT CAT CGG ATG		576
Asp Cys Asn Cys Ser Ile Tyr Thr Gly His Ile Thr Gly His Arg Met		
180	185	190
GCA		579
Ala		

(2) INFORMATION FOR SEQ ID NO: 168:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 193 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala		
1	5	10
		15

Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val
20 25 30

Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe
35 40 45

Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Thr Ser
50 55 60

Ala Val Asn Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile Thr Asn Asp
65 70 75 80

Cys Pro Asn Ala Ser Ile Val Tyr Glu Thr Glu Asn His Ile Leu His
85 90 95

Leu Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Gln Ser Arg Cys
100 105 110

Tyr Val Ala Leu Thr Pro Thr Val Ala Ser Pro Tyr Ala Gly Ala Pro
115 120 125

Leu Glu Pro Leu Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr
130 135 140

Met Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Leu Phe Leu
145 150 155 160

Val Gly Gln Met Phe Thr Phe Gln Pro Arg Arg His Tyr Thr Thr Gln
165 170 175

Asp Cys Asn Cys Ser Ile Tyr Thr Gly His Ile Thr Gly His Arg Met
180 185 190

Ala

(2) INFORMATION FOR SEQ ID NO: 169:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 579 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 1..579

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
(B) LOCATION: 1..576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

ACA TGC GGC TTC GCC GAC CTC ATG GGA TAC ATC CCG CTT GTA GGC GCC	48
Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala	
1 5 10 15	
CCC GTG GGT GGC GTC GCC AGA GCC CTG GCA CAC GGT GTT AGG GCT GTG	96
Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val	
20 25 30	
GAA GAC GGG ATC AAC TAC GCA ACA GGG AAT CTC CCC GGT TGC TCC TTT	144
Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe	
35 40 45	
TCT ATC TTC CTC TTG GCA CTT CTC TCG TGC CTC ACT GTT CCC GCG TCG	192
Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser	
50 55 60	
GGC GTT AAC TAT CGC AAT GCT TCG GGC GTT TAT CAC ATC ACC AAC GAC	240
Gly Val Asn Tyr Arg Asn Ala Ser Gly Val Tyr His Ile Thr Asn Asp	
65 70 75 80	
TGC CCG AAT GCG AGC ATA GTG TAC GAG ACC GAC AAT GAC ATC TTA CAC	288
Cys Pro Asn Ala Ser Ile Val Tyr Glu Thr Asp Asn His Ile Leu His	
85 90 95	
CTC CCA GGG TGC GTA CCC TGT GTG AAG ACC GGG AAC CAG TCG CGG TGT	336
Leu Pro Gly Cys Val Pro Cys Val Lys Thr Gly Asn Gln Ser Arg Cys	
100 105 110	
TGG GTG GCC CTC ACT CCC ACA GTG GCG TCG CCT TAC GTC GGT GCT CCG	384
Trp Val Ala Leu Thr Pro Thr Val Ala Ser Pro Tyr Val Gly Ala Pro	
115 120 125	
CTC GAG CCC TTG CGG CGC CAT GTG GAC CTG ATG GTA GGT GCT GCC ACC	432
Leu Glu Pro Leu Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr	
130 135 140	
GTG TGC TCC GCC CTC TAC GTC GGC GAC CTG TGC GGT GGC TTA TTC TTG	480
Val Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys Gly Gly Leu Phe Leu	
145 150 155 160	
GTA GGC CAA ATG TTC ACC TTC CAA CCG CGA CGC CAC TGG ACG ACC CAG	528
Val Gly Gln Met Phe Thr Phe Gln Pro Arg Arg His Trp Thr Thr Gln	
165 170 175	
GAC TGT AAT TGT TCC ATC TAC GCA GGG CAT ATT ACG GGC CAT CGG ATG	576
Asp Cys Asn Cys Ser Ile Tyr Ala Gly His Ile Thr Gly His Arg Met	
180 185 190	
GCT	579
Ala	

(2) INFORMATION FOR SEQ ID NO: 170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala
1 5 10 15

Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val
20 25 30

Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe
35 40 45

Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser
50 55 60

Gly Val Asn Tyr Arg Asn Ala Ser Gly Val Tyr His Ile Thr Asn Asp
65 70 75 80

Cys Pro Asn Ala Ser Ile Val Tyr Glu Thr Asp Asn His Ile Leu His
85 90 95

Leu Pro Gly Cys Val Pro Cys Val Lys Thr Gly Asn Gln Ser Arg Cys
100 105 110

Trp Val Ala Leu Thr Pro Thr Val Ala Ser Pro Tyr Val Gly Ala Pro
115 120 125

Leu Glu Pro Leu Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr
130 135 140

Val Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys Gly Gly Leu Phe Leu
145 150 155 160

Val Gly Gln Met Phe Thr Phe Gln Pro Arg Arg His Trp Thr Thr Gln
165 170 175

Asp Cys Asn Cys Ser Ile Tyr Ala Gly His Ile Thr Gly His Arg Met
180 185 190

Ala

(2) INFORMATION FOR SEQ ID NO: 171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..579

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

ACA TGC GGC TTC GCC GAC CTC ATG GGA TAC ATC CCG CTT GTG GGC GCC	48
Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala	
1 5 10 15	
CCT GTT GGT GGC GTC GCC AGA GCC CTT GCG CAC GGC GTC AGG GCT GTG	96
Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val	
20 25 30	
GAA GAC GGG ATT AAC TAT GCA ACA GGG AAC CTT CCT GGT TGC TCC TTT	144
Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe	
35 40 45	
TCT ATC TTC CTT CTG GCA CTT CTC TCG TGC CTG ACT GTC CCC GCC TCG	192
Ser Ile Phe Leu Leu Ala Leu Ser Cys Leu Thr Val Pro Ala Ser	
50 55 60	
GCT GTG CAT TAT CAC AAC ACC TCG GGC ATC TAC CAC CTC ACC AAT GAC	240
Ala Val His Tyr His Asn Thr Ser Gly Ile Tyr His Leu Thr Asn Asp	
65 70 75 80	
TGC CCT AAC TCT AGC ATA GTC TTT GAG GCA GTC CAT CAC ATC TTG CAC	288
Cys Pro Asn Ser Ser Ile Val Phe Glu Ala Val His His Ile Leu His	
85 90 95	
CTT CCA GGA TGC CCT TGT GTA AGA ACT GGG AAC CAG TCT CGG TGC	336
Leu Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Gln Ser Arg Cys	
100 105 110	
TGG GTA GCC TTG ACC CCC ACG CTG GCC GCG CCA TAC CTT GGC GCT CCA	384
Trp Val Ala Leu Thr Pro Thr Leu Ala Ala Pro Tyr Leu Gly Ala Pro	
115 120 125	
CTC GAG TCC ATG CGG CGT CAC GTG GAT TTG ATG GTG GGC ACT GCT ACA	432
Leu Glu Ser Met Arg Arg His Val Asp Leu Met Val Gly Thr Ala Thr	
130 135 140	
TTG TGC TCA GCA CTC TAC GTT GGG GAC CTG TGC GGG GGC ATA TTC CTA	480
Leu Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys Gly Gly Ile Phe Leu	
145 150 155 160	
GCG GGC CAG ATG TTC ACC TTC CGG CCC CGC CTC CAT TGG ACC ACC CAG	528
Ala Gly Gln Met Phe Thr Phe Arg Pro Arg Leu His Trp Thr Thr Gln	
165 170 175	

GAG TGC AAT TGT TCC ACC TAT CCG GGC CAC ATC ACG GGT CAT AGA ATG	576	
Glu Cys Asn Cys Ser Thr Tyr Pro Gly His Ile Thr Gly His Arg Met		
180	185	190

GCG	579
Ala	

(2) INFORMATION FOR SEQ ID NO: 172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala			
1	5	10	15

Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val			
20	25	30	

Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe			
35	40	45	

Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser			
50	55	60	

Ala Val His Tyr His Asn Thr Ser Gly Ile Tyr His Leu Thr Asn Asp			
65	70	75	80

Cys Pro Asn Ser Ser Ile Val Phe Glu Ala Val His His Ile Leu His			
85	90	95	

Leu Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Gln Ser Arg Cys			
100	105	110	

Trp Val Ala Leu Thr Pro Thr Leu Ala Ala Pro Tyr Leu Gly Ala Pro			
115	120	125	

Leu Glu Ser Met Arg Arg His Val Asp Leu Met Val Gly Thr Ala Thr			
130	135	140	

Leu Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys Gly Gly Ile Phe Leu			
145	150	155	160

Ala Gly Gln Met Phe Thr Phe Arg Pro Arg Leu His Trp Thr Thr Gln			
165	170	175	

Glu Cys Asn Cys Ser Thr Tyr Pro Gly His Ile Thr Gly His Arg Met			
180	185	190	

Ala

(2) INFORMATION FOR SEQ ID NO: 173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..579

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

ACG TGC GGT TCC GCC GAC CTC ATG GGA TAC ATC CCG CTC GTA GGC GCC	48
Thr Cys Gly Ser Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala	
1 5 10 15	
CCT GTG GGT GGC GTC GCC AGG GCC TTG GCG CAT GGC GTC AGG GCT GTG	96
Pro Val Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val	
20 25 30	
GAG GAC GGG ATA AAC TAT GCA ACA GGG AAC CTT CCT GGT TGC TCT TTT	144
Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe	
35 40 45	
TCT ATC TTC CTT CTG GCA CTT CTC TCG TGC CTG ACT GTC CCC GCC TCA	192
Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser	
50 55 60	
GCT GTG CAT TAT CAC AAC ACC TCG GGC ATC TAT CAC ATC ACT AAT GAC	240
Ala Val His Tyr His Asn Thr Ser Gly Ile Tyr His Ile Thr Asn Asp	
65 70 75 80	
TGC CCT AAC TCT AGC ATA GTC TTT GAG GCA GAG CAT CAC ATC TTG CAT	288
Cys Pro Asn Ser Ser Ile Val Phe Glu Ala Glu His His Ile Leu His	
85 90 95	
CTT CCA GGA TGC GTC CCC TGT GTG AGA ACT GGG AAC CAG TCA CGA TGC	336
Leu Pro Gly Cys Val Pro Cys Val-Arg Thr Gly Asn Gln Ser Arg Cys	
100 105 110	
TGG ATA GCC TTG ACC CCT ACG TTG GGC GCG CCA CAC ATT GGC GCT CCA	384
Trp Ile Ala Leu Thr Pro Thr Leu Ala Ala Pro His Ile Gly Ala Pro	

115	120	125	
CTT GAG TCC ATG CGA CGT CAT GTG GAT TTG ATG GTA GGC ACT GCC ACA			432
Leu Glu Ser Met Arg Arg His Val Asp Leu Met Val Gly Thr Ala Thr			
130	135	140	
TTG TGC TCC GCA CTC TAC ATT GGA GAT CTG TGC GGA GGC ATA TTT CTA			480
Leu Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Ile Phe Leu			
145	150	155	160
GTG GGC CAG ATG TTC AAC TTC AGG CCC CGC CTG CAC TGG ACC ACC CAG			528
Val Gly Gln Met Phe Asn Phe Arg Pro Arg Leu His Trp Thr Thr Gln			
165	170	175	
GAG TGC AAT TGT TCC ATC TAT CCA GGC CAC ATC ACG GGT CAC AGA ATG			576
Glu Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg Met			
180	185	190	
CGC			579
Ala			

(2) INFORMATION FOR SEQ ID NO: 174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

Thr Cys Gly Ser Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala
 1 5 10 15

Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val
 20 25 30

Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe
 35 40 45

Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser
 50 55 60

Ala Val His Tyr His Asn Thr Ser Gly Ile Tyr His Ile Thr Asn Asp
 65 70 75 80

Cys Pro Asn Ser Ser Ile Val Phe Glu Ala Glu His His Ile Leu His
 85 90 95

Leu Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Gln Ser Arg Cys
 100 105 110

Trp Ile Ala Leu Thr Pro Thr Leu Ala Ala Pro His Ile Gly Ala Pro
 115 120 125

224

Leu Glu Ser Met Arg Arg His Val Asp Leu Met Val Gly Thr Ala Thr
 130 135 140

Leu Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Ile Phe Leu
 145 150 155 160

Val Gly Gln Met Phe Asn Phe Arg Pro Arg Leu His Trp Thr Thr Gln
 165 170 175

Glu Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg Met
 180 185 190

Ala

(2) INFORMATION FOR SEQ ID NO: 175:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 579 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..579
- (ix) FEATURE:
 - (A) NAME/KEY: mat_peptide
 - (B) LOCATION: 1..576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:

ACG TGC GGC TTT GCC GAC CTC ATG GGA TAC ATC CCG CTC GTG GGC GCC	48
Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala	
1 5 10 15	
CCT GTG GGT GGC GTC GCC AGG GCC TTG GCA CAT GGT GTC AGG GCC GTG	96
Pro Val Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val	
20 25 30	
GAG GAC GGG ATT AAC TAT GCA ACA GGG AAT CTT CCC GGT TGC TCC TTT	144
Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe	
35 40 45	
TCT ATC TTC CTT CTA GCA CTT CTC TCG TGC TTG ACT GTC CCG GCC TCG	192
Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser	
50 55 60	
GCG CAG CAC TAC CGG AAC ATC TCG GGC ATT TAT CAC GTC ACC AAT GAC	240
Ala Gln His Tyr Arg Asn Ile Ser Gly Ile Tyr His Val Thr Asn Asp	

225

65	70	75	80	
TGC CCG AAC TCT AGT ATA GTG TAT GAA GCT GAC CAT CAT ATC ATG CAT				288
Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Met His				
85	90	95		
CTA CCA GGG TGT GTG CCT TGC GTG AGA ACC GGG AAC ACC TCG CGC TGC				336
Leu Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Thr Ser Arg Cys				
100	105	110		
TGG GTT CCT TTA ACA CCC ACT GTG GCT GCC CCC TAT GTT GGC GCG CCG				384
Trp Val Pro Leu Thr Pro Thr Val Ala Ala Pro Tyr Val Gly Ala Pro				
115	120	125		
CTC GAA TCC ATG CGG CGG CAC GTG GAC TTA ATG GTG GGT GCC GCC ACC				432
Leu Glu Ser Met Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr				
130	135	140		
GTC TGC TCG GCC CTG TAC ATC GGA GAC CTT TGC GGA GGT GTC TTC CTG				480
Val Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu				
145	150	155	160	
GTC GGG CAG ATG TTC ACC TTC CGG CCG CGC CGC CAT TGG ACT ACC CAG				528
Val Gly Gln Met Phe Thr Phe Arg Pro Arg Arg His Trp Thr Thr Gln				
165	170	175		
GAC TGC AAC TGC TCT ATC TAT GAT GGC CAC ATC ACC GGC CAT AGA ATG				576
Asp Cys Asn Cys Ser Ile Tyr Asp Gly His Ile Thr Gly His Arg Met				
180	185	190		
GCT				579
Ala				

(2) INFORMATION FOR SEQ ID NO: 176:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala			
1	5	10	15
Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val			
20	25	30	
Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe			
35	40	45	
Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser			
50	55	60	

Ala Gln His Tyr Arg Asn Ile Ser Gly Ile Tyr His Val Thr Asn Asp
 65 70 75 80
 Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Met His
 '85 90 95
 Leu Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Thr Ser Arg Cys
 100 105 110
 Trp Val Pro Leu Thr Pro Thr Val Ala Ala Pro Tyr Val Gly Ala Pro
 115 120 125
 Leu Glu Ser Met Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr
 130 135 140
 Val Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu
 145 150 155 160
 Val Gly Gln Met Phe Thr Phe Arg Pro Arg Arg His Trp Thr Thr Gln
 165 170 175
 Asp Cys Asn Cys Ser Ile Tyr Asp Gly His Ile Thr Gly His Arg Met
 180 185 190
 Ala

(2) INFORMATION FOR SEQ ID NO: 177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..579

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

ACG TGC GGG TTC GCC GAC CTC ATG GGA TAC ATC CCG CTC GTG GGC GCT
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala
 1 5 10 15

48

CCA GTA GGA GGC GTC GCC AGA GCC TTG GCG CAT GGC GTC AGG GCT GTG
 Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val

96

227

	20	25	30	
GAG GAC GGG ATC AAT TAC GCA ACA GGG AAC CTT CCC GGC TGC TCC TTT				144
Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe				
35	40	45		
TCT ATC TTC CTC TTG GTA CTT CTC TCG CGC CTA ACT GTC CCA GCG TCT				192
Ser Ile Phe Leu Leu Val Leu Leu Ser Arg Leu Thr Val Pro Ala Ser				
50	55	60		
GCT CAG CAC TAC CGG AAT GCA TCG GGC ATC TAC CAT GTC ACC AAC GAC				240
Ala Gln His Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp				
65	70	75	80	
TGC CCG AAC TCC AGT ATT GTG TAT GAA GCC GAC CAT CAC ATC ATG CAC				288
Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Met His				
85	90	95		
CTA CCC GGG TGT GTG CCC TGT GTA AGA ACT GGG AAT GTC TCG CGT TGC				336
Leu Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Val Ser Arg Cys				
100	105	110		
TGG ATT CCT TTA ACA CCC ACT GTA GCC GTC CCC TAC CTC GGG GCT CCA				384
Trp Ile Pro Leu Thr Pro Thr Val Ala Val Pro Tyr Leu Gly Ala Pro				
115	120	125		
CTT ACG TCT GTA CGG CAG CAT GTG GAC CTG ATG GTG GGG GCG GCC ACC				432
Leu Thr Ser Val Arg Gln His Val Asp Leu Met Val Gly Ala Ala Thr				
130	135	140		
TTA TGC TCT GCC CTC TAC GGA GAC CAT TGC GGA GGT GTC TTC TTG				480
Leu Cys Ser Ala Leu Tyr Ile Gly Asp His Cys Gly Gly Val Phe Leu				
145	150	155	160	
GCA GGG CAG ATG GTC AGT TTC CAA CCC CGG CGT CAT TGG ACT ACC CAG				528
Aia Gly Gln Met Val Ser Phe Gln Pro Arg Arg His Trp Thr Gln				
165	170	175		
GAT TGC AAC TGT TCC ATC TAT GTG GGC CAC ATC ACC GGC CAC AGG ATG				576
Asp Cys Asn Cys Ser Ile Tyr Val Gly His Ile Thr Gly His Arg Met				
180	185	190		
GCC				579
Ala				

(2) INFORMATION FOR SEQ ID NO: 178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178:

228

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala
1 5 10 15

Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val
20 25 30

Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe
35 40 45

Ser Ile Phe Leu Leu Val Leu Ser Arg Leu Thr Val Pro Ala Ser
50 55 60

Ala Gln His Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp
65 70 75 80

Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Met His
85 90 95

Leu Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Val Ser Arg Cys
100 105 110

Trp Ile Pro Leu Thr Pro Thr Val Ala Val Pro Tyr Leu Gly Ala Pro
115 120 125

Leu Thr Ser Val Arg Gln His Val Asp Leu Met Val Gly Ala Ala Thr
130 135 140

Leu Cys Ser Ala Leu Tyr Ile Gly Asp His Cys Gly Gly Val Phe Leu
145 150 155 160

Ala Gly Gln Met Val Ser Phe Gln Pro Arg Arg His Trp Thr Thr Gln
165 170 175

Asp Cys Asn Cys Ser Ile Tyr Val Gly His Ile Thr Gly His Arg Met
180 185 190

Ala

(2) INFORMATION FOR SEQ ID NO: 179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..579

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

ACCTGCGGCT TCGCCGACCT CATGGGATAC ATCCCGCTCG TAGGCGCCCC CGTGGGAGGC	60
GTCGCCAGAR CTCTGGCGCA TGGCGTCAGG GCTCTGGAAG ACGGGATCAA TTATGCAACA	120
GGGAATCTTC CTGGTTGCTC TTTCTCTATC TCCCTTCTTG AACTTCTCTC GTGCCTGACT	180
GTTCCCGCCT CAGCCATCCA CTATGCAAT GCTTCGGACG GTTATTATAT CACCAATGAT	240
TGCCCGAACT CTAGCATAGT GTATGAAGCC GAGAACACCA TCTTGCACCT TCCGGGGTGT	300
ATACCCCTGTG TGAAGACCGG GAATCAGTCG CGGTGCTGGG TGGCTCTCAC CCCCACGCTG	360
GCGGCCAAC ACCTACGTGC TCCGCTTTCG TCCTTACGGG CGCATGTGGA CCTAATGGTG	420
GGGGCCGCCA CGGCATGCTC CGCTTTTAC ATTGGAGATC TGTGCGGGGG TGTGTTTTG	480
GCGGGCCAAC TGTTCACTAT CCGGCCACGC ATTCAATGAAA CCACTCAGGA CTGCAATTGC	540
TCCATCTACT CAGGGCACAT CACGGTNNN NNNNNNNNN	579

(2) INFORMATION FOR SEQ ID NO: 180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180:

Thr	Cys	Gly	Phe	Ala	Asp	Leu	Met	Gly	Tyr	Ile	Pro	Leu	Val	Gly	Ala	
1																15

Pro	Val	Gly	Gly	Val	Ala	Arg	Xaa	Leu	Ala	His	Gly	Val	Arg	Ala	Leu
															30
20															

Glu	Asp	Gly	Ile	Asn	Tyr	Ala	Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe
35															45

Ser	Ile	Ser	Leu	Leu	Glu	Leu	Leu	Ser	Cys	Leu	Thr	Val	Pro	Ala	Ser
50															60

Ala	Ile	His	Tyr	Arg	Asn	Ala	Ser	Asp	Gly	Tyr	Tyr	Ile	Thr	Asn	Asp
65															80

Cys	Pro	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	Glu	Asn	His	Ile	Leu	His
85															95

Leu	Pro	Gly	Cys	Ile	Pro	Cys	Val	Lys	Thr	Gly	Asn	Gln	Ser	Arg	Cys
100															110

Trp Val Ala Leu Thr Pro Thr Leu Ala Ala Pro His Leu Arg Ala Pro			
115	120	125	
Leu Ser Ser Leu Arg Ala His Val Asp Leu Met Val Gly Ala Ala Thr			
130	135	140	
Ala Cys Ser Ala Phe Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu			
145	150	155	160
Ala Gly Gln Leu Phe Thr Ile Arg Pro Arg Ile His Glu Thr Thr Gln			
165	170	175	
Asp Cys Asn Cys Ser Ile Tyr Ser Gly His Ile Thr Gly Xaa Xaa Xaa			
180	185	190	
Xaa			

(2) INFORMATION FOR SEQ ID NO: 181:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 579 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - iii) HYPOTHETICAL: NO
 - iii) ANTI-SENSE: NO
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..578

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

GCGTGC GGCT TCGCCGATCT CATGGGATAC ATCCC GCTCG TAGGCG CCCC CGTGGG TG GC	60
GTCGCCAGAG CCCTGGCGCA CGGTGTTAGG GCTGTGGAGG ACGGGATTAA CTACGCAACA	120
GGGAATCTTC CTGGTTGCTC TTTCTCTATC TNCC TTCTGG CACTTCTCTC GTGCCTGACT	180
GTCCC GGCCCT CGGCTCAGCA CTACCGGAAT GTCTGGGCA TCTACCACGT CACCAATGAT	240
TGCCCGAATT CCAGCATAGT GTATGAAGCC GATCACCAACA TCATGCAC TT ACCAGGGTG C	300
ATACCCCTGCG TGAGGACCGG GAACGTTTCG CGCTGCTGGG TATCTCTGAC ACCTACTGTG	360
GCTGCTCCCT ACCTCGGGGC TCCGCTTACG TCGCTACGGC GGCATGTGGA TTTGATGGTG	420
GGTGCAGGCCA CCCTTTGCTC TGCCCTCTAC GTCGGAGACC TCTGTGGAGG TGTCTT CCTA	480

GTGGGACAGA TGTTCACCTT CCAGCCGC CGCCACTGGA CCACTCAGGA CTGCAACTGC 540
TCCATTTACG TCGGCCACAT CACAGGCCAC AGAATGGCT 579

(2) INFORMATION FOR SEQ ID NO: 182:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 193 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:

Ala Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala
1 5 10 15
Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val
20 25 30
Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe
35 40 45
Ser Ile Xaa Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser
50 55 60
Ala Gln His Tyr Arg Asn Val Ser Gly Ile Tyr His Val Thr Asn Asp
65 70 75 80
Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Met His
85 90 95
Leu Pro Gly Cys Ile Pro Cys Val Arg Thr Gly Asn Val Ser Arg Cys
100 105 110
Trp Val Ser Leu Thr Pro Thr Val Ala Ala Pro Tyr Leu Gly Ala Pro
115 120 125
Leu Thr Ser Leu Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr
130 135 140
Leu Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys Gly Gly Val Phe Leu
145 150 155 160
Val Gly Gln Met Phe Thr Phe Gln Pro Arg Arg His Trp Thr Thr Gln
165 170 175
Asp Cys Asn Cys Ser Ile Tyr Val Gly His Ile Thr Gly His Arg Met
180 185 190
Ala

(2) INFORMATION FOR SEQ ID NO: 183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..579

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..579

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

ACC TGC GGC TTT GCC GAC CTC ATG GGA TAC ATC CCG CTC GTA GGC GCC Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala	48
1 5 10 15	
CCT GTG GGT GGC GTC GCC AGG GCC CTA GAA CAC GGT GTT AGG GCT GTG Pro Val Gly Val Ala Arg Ala Leu Glu His Gly Val Arg Ala Val	96
20 25 30	
GAG GAC GGT ATT AAT TAT GCA ACA GGG AAT CTC CCC GGT TGC TCT TTT Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe	144
35 40 45	
TCT ATC TCC CTC TTG GCA CTT CTT TCG TGC CTG ACT GTT CCC ACC TCA Ser Ile Ser Leu Leu Ala Leu Ser Cys Leu Thr Val Pro Thr Ser	192
50 55 60	
GCC GTC AAC TAT CGC AAC GCC TCG GGC GTC TAT CAT ATC ACC AAT GAC Ala Val Asn Tyr Arg Asn Ala Ser Gly Val Tyr His Ile Thr Asn Asp	240
65 70 75 80	
TGC CCG AAT TCG AGC ATA GTG TAC GAG GCT GAC TAC CAC ATC CTA CAC Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Tyr His Ile Leu His	288
85 90 95	
CTC CCT GGG TGC TTA CCC TGC GTG AGG GTT GGG AAT CAG TCA CGC TGC Leu Pro Gly Cys Leu Pro Cys Val Arg Val Gly Asn Gln Ser Arg Cys	336
100 105 110	
TGG GTG GCC CTT ACT CCC ACC GTG GCG GCG CCT TAC GTT GGT GCT CCG Trp Val Ala Leu Thr Pro Thr Val Ala Ala Pro Tyr Val Gly Ala Pro	384

115	120	125	
CTA GAA TCC CTC CGG AGT CAT GTG GAT CTG ATG GTA GGT GCT GCT ACT Leu Glu Ser Leu Arg Ser His Val Asp Leu Met Val Gly Ala Ala Thr			432
130	135	140	
GTG TGC TCC GCT CTT TAC ATC GGG GAC CTG TGC GGT GGC GTA TTT TTG Val Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu			480
145	150	155	160
GTT GGT CAG ATG TTT TCT TTC CAG CCG CGA CGC CAC TGG ACC ACG CAG Val Gly Gln Met Phe Ser Phe Gln Pro Arg Arg His Trp Thr Thr Gln			528
165	170	175	
GAC TGC AAT TGT TCT ATC TAC GCG GGG CAC GTT ACG GGC CAC AGG ATG Asp Cys Asn Cys Ser Ile Tyr Ala Gly His Val Thr Gly His Arg Met			576
180	185	190	
GCA			- 579
Ala			

(2) INFORMATION FOR SEQ ID NC: 184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala			
1	5	10	15
Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val			
20	25	30	
Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe			
35	40	45	
Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Thr Ser			
50	55	60	
Ala Val Asn Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile Thr Asn Asp			
65	70	75	80
Cys Pro Asn Ala Ser Ile Val Tyr Glu Thr Glu Asn His Ile Leu His			
85	90	95	
Leu Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Gln Ser Arg Cys			
100	105	110	
Trp Val Ala Leu Thr Pro Thr Val Ala Ser Pro Tyr Ala Gly Ala Pro			
115	120	125	
Leu Glu Pro Leu Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr			
130	135	140	

235

180

185

190

(2) INFORMATION FOR SEQ ID NO: 185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..579

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185:

ACT TGC GGC TTT GCC GAC CTC ATG GGA TAC ATC CCG CTC GTA GGC GCC	48
Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala	
1 5 10 15	
CCC GTG GGT GGC GTC GCC AGA GCC CTG GAA CAT GGT GTT AGG GCT GTG	96
Pro Val Gly Gly Val Ala Arg Ala Leu Glu His Gly Val Arg Ala Val	
20 25 30	
GAG GAC GGC ATC AAT TAT GCA ACA GGG AAT CTC CCC GGT TGC TCT TTC	144
Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe	
35 40 45	
TCT ATC TAC CTC TTG GCA CTT CTC TCG TGC CTG ACT GTT CCC ACC TCG	192
Ser Ile Tyr Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Thr Ser	
50 55 60	
GCC ATC CAC TAT CGC AAT GCC TCG GGC GTC TAC CAC GTC ACC AAT GAC	240
Ala Ile His Tyr Arg Asn Ala Ser Gly Val Tyr His Val Thr Asn Asp	
65 70 75 80	
TGC CCG AAC TCG AGC ATA GTG TAC GAG GCC GAC CAC CAC ATC CTA CAC	288
Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Leu His	
85 90 95	
CTT CCA GGG TGC TTA CCC TGT GTG AGG GTT GGG AAT CAG TCA CGT TGT	336
Leu Pro Gly Cys Leu Pro Cys Val Arg Val Gly Asn Gln Ser Arg Cys	
100 105 110	
TGG GTG GCC CTC TCT CCC ACC GTG GCG GCG CCT TAC ATC GGT GCT CCA	384

Trp Val Ala Leu Ser Pro Thr Val Ala Ala Pro Tyr Ile Gly Ala Pro			
115	120	125	
GTT GAA TCC TTC CGG AGA CAC GTG GAC ATG ATG GTG GGC GCT GCT ACT			432
Val Glu Ser Phe Arg Arg His Val Asp Met Met Val Gly Ala Ala Thr			
130	135	140	
GTG TGC TCC GCT CTC TAT ATT GGG GAC TTG TGT GGT GGC GCA TTC TTG			480
Val Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu			
145	150	155	160
GTT GGT CAG ATG TTT TCT TTC CGG CCA CGA CGC CAC TGG ACT ACG CAG			528
Val Gly Gln Met Phe Ser Phe Arg Pro Arg Arg His Trp Thr Thr Gln			
165	170	175	
GAC TGC AAT TGT TCC ATC TAC GCG GGG CAC ATC ACT GGC CAC GGA ATG			576
Asp Cys Asn Cys Ser Ile Tyr Ala Gly His Ile Thr Gly His Gly Met			
180	185	190	
GCA			579
Ala			

(2) INFORMATION FOR SEQ ID NO: 186:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 193 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala			
1	5	10	15
Pro Val Gly Gly Val Ala Arg Ala Leu Glu His Gly Val Arg Ala Val			
20	25	30	
Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe			
35	40	45	
Ser Ile Tyr Leu Leu Ala Leu Ser Cys Leu Thr Val Pro Thr Ser			
50	55	60	
Ala Ile His Tyr Arg Asn Ala Ser Gly Val Tyr His Val Thr Asn Asp			
65	70	75	80
Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Leu His			
85	90	95	
Leu Pro Gly Cys Leu Pro Cys Val Arg Val Gly Asn Gln Ser Arg Cys			
100	105	110	
Trp Val Ala Leu Ser Pro Thr Val Ala Ala Pro Tyr Ile Gly Ala Pro			
115	120	125	

Val Glu Ser Phe Arg Arg His Val Asp Met Met Val Gly Ala Ala Thr
130 135 140

Val Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu
145 150 155 160

Val Gly Gln Met Phe Ser Phe Arg Pro Arg Arg His Trp Thr Thr Gln
165 170 175

Asp Cys Asn Cys Ser Ile Tyr Ala Gly His Ile Thr Gly His Gly Met
180 185 190

Ala

(2) INFORMATION FOR SEQ ID NO: 187:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 579 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 1..579

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
 (B) LOCATION: 1..576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187:

ACT TGC GGC TTT GCC GAC CTC ATG GGA TAC ATC CCG CTC GTA GGC GCC	48
Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala	
1 5 10 15	

CCT GTG GGT GGC GTC GCC AGG GCC CTG GCA CAC GGT GTT AGG GCT GTG	96
Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val	
20 25 30	

GAG GAC GGG ATC AAT TAT GCG ACA GGG AAT CTT CCC GGT TGC TCT TTC	144
Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe	
35 40 45	

TCT ATC TTC CTC TTG GCA CTT CTT TCG TGC CTG ACT GTT CCC ACC TCG	192
Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Thr Ser	
50 55 60	

GCC GTC AAC TAT CGC AAT GCC TCG GGC ATC TAT CAC ATC ACC AAT GAC	240
---	-----

Ala Val Asn Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile Thr Asn Asp				
65	70	75	80	
TGC CCG AAC TCG AGC ATA GTG TAC GAG ACC GAG CAC CAC ATC CTA CAC				288
Cys Pro Asn Ser Ser Ile Val Tyr Glu Thr Glu His His Ile Leu His				
85	90	95		
CTC CCA GGG TGT TTA CCC TGC GTG AGG GTT GGG AAT CAG TCA CGC TGC				336
Leu Pro Gly Cys Leu Pro Cys Val Arg Val Gly Asn Gln Ser Arg Cys				
100	105	110		
TGG GTG GCC CTC ACT CCC ACC GTG GCG GCG CCT TAC ATC GGC GCT CCG				384
Trp Val Ala Leu Thr Pro Thr Val Ala Ala Pro Tyr Ile Gly Ala Pro				
115	120	125		
CTT GAA TCC CTC CGG AGT CAT GTG GAT CTG ATG GTA GGT GCC GCT ACT				432
Leu Glu Ser Leu Arg Ser His Val Asp Leu Met Val Gly Ala Ala Thr				
130	135	140		
GCG TGC TCC GCT CTT TAC ATC GGA GAC CTG TGC GGT GGC GTA TTT TTG				480
Ala Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu				
145	150	155	160	
GTT GGT CAG ATG TTC TCT TTC CAG CGG CGG CGC CAC TGG ACT ACG CAG				528
Val Gly Gln Met Phe Ser Phe Gln Pro Arg Arg His Trp Thr Thr Gln				
165	170	175		
GAC TGC AAT TGT TCC ATC TAC GCG GGG CAC GTT ACG GGC CAC AGG ATG				576
Asp Cys Asn Cys Ser Ile Tyr Ala Gly His Val Thr Gly His Arg Met				
180	185	190		
GCA				579
Ala				

(2) INFORMATION FOR SEQ ID NO: 188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala				
1	5	10	15	
Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val				
20	25	30		
Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe				
35	40	45		
Ser Ile Phe Leu Leu Ala Leu Ser Cys Leu Thr Val Pro Thr Ser				
50	55	60		

Ala Val Asn Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile Thr Asn Asp
 65 70 75 80

 Cys Pro Asn Ser Ser Ile Val Tyr Glu Thr Glu His His Ile Leu His
 85 90 95

 Leu Pro Gly Cys Leu Pro Cys Val Arg Val Gly Asn Gln Ser Arg Cys
 100 105 110

 Trp Val Ala Leu Thr Pro Thr Val Ala Ala Pro Tyr Ile Gly Ala Pro
 115 120 125

 Leu Glu Ser Leu Arg Ser His Val Asp Leu Met Val Gly Ala Ala Thr
 130 135 140

 Ala Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu
 145 150 155 160

 Val Gly Gln Met Phe Ser Phe Gln Pro Arg Arg His Trp Thr Thr Gln
 165 170 175

 Asp Cys Asn Cys Ser Ile Tyr Ala Gly His Val Thr Gly His Arg Met
 180 185 190

 Ala

(2) INFORMATION FOR SEQ ID NO: 189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..579

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

ACG TGC GGC TTC GCC GAC CTC ATG GGA TAC ATC CCG CTC GTG GGC GCC
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala
 1 5 10 15

48

CCC GTT GGG GGC GTC GCC AGG GCC CTG GCG CAT GGC GTC AGG GCT GTG Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val 20 25 30	96
GAG GAC GGG ATT AAC TAT GCG ACA GGG AAT CTT CCC GGT TGC TCT TTC Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe 35 40 45	144
TCT ATC TTC CTC CTG GCA CTT CTT TCG TGC CTC ACT GTC CCA GCG TCA Ser Ile Phe Leu Leu Ala Leu Ser Cys Leu Thr Val Pro Ala Ser 50 55 60	192
GCT GAG CAC TAC CGG AAT GCT TCG GGC ATC TAT CAC ATC ACC AAT GAC Ala Glu His Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile Thr Asn Asp 65 70 75 80	240
TGT CCG AAT TCC AGC GTA GTC TAT GAA ACT GAC CAC CAT ATA TTG CAC Cys Pro Asn Ser Ser Val Val Tyr Glu Thr Asp His His Ile Leu His 85 90 95	288
TTG CCG GGG TGC GTA CCC TGC GTG AGG GCC GGG AAC GTG TCT CGT TGC Leu Pro Gly Cys Val Pro Cys Val Arg Ala Gly Asn Val Ser Arg Cys 100 105 110	336
TGG ACG CCG GTA ACA CCT ACG GTG GCT GCC GTA TCC ATG GAC GCT CCG Trp Thr Pro Val Thr Pro Val Ala Ala Val Ser Met Asp Ala Pro 115 120 125	384
CTC GAG TCC TTC CGG CGG CAT GTG GAC CTA ATG GTA GGT GCG GCC ACC Leu Glu Ser Phe Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr 130 135 140	432
GTG TGT TCT GTC CTC TAT GTT GGA GAC CTC TGT GGA GGT GCT TTC CTA Val Cys Ser Val Leu Tyr Val Gly Asp Leu Cys Gly Gly Ala Phe Leu 145 150 155 160	480
GTG GGG CAG ATG TTC ACC TTC CAG CCG CGT CGC CAC TGG ACC ACG CAG Val Gly Gln Met Phe Thr Phe Gln Pro Arg Arg His Trp Thr Thr Gln 165 170 175	528
GAT TGT AAT TGC TCC ATC TAT ACT GGC CAT ATC ACC GGC CAC AGG ATG Asp Cys Asn Cys Ser Ile Tyr Thr Gly His Ile Thr Gly His Arg Met 180 185 190	576
GGC Ala	579

(2) INFORMATION FOR SEQ ID NO: 190:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 193 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala
1 5 10 15

Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val
20 25 30

Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe
35 40 45

Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser
50 55 60

Ala Glu His Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile Thr Asn Asp
65 70 75 80

Cys Pro Asn Ser Ser Val Val Tyr Glu Thr Asp His His Ile Leu His
85 90 95

Leu Pro Gly Cys Val Pro Cys Val Arg Ala Gly Asn Val Ser Arg Cys
100 105 110

Trp Thr Pro Val Thr Pro Thr Val Ala Ala Val Ser Met Asp Ala Pro
115 120 125

Leu Glu Ser Phe Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr
130 135 140

Val Cys Ser Val Leu Tyr Val Gly Asp Leu Cys Gly Gly Ala Phe Leu
145 150 155 160

Val Gly Gln Met Phe Thr Phe Gln Pro Arg Arg His Trp Thr Thr Gln
165 170 175

Asp Cys Asn Cys Ser Ile Tyr Thr Gly His Ile Thr Gly His Arg Met
180 185 190

Ala

(2) INFORMATION FOR SEQ ID NO: 191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS

(B) LOCATION: 1..289

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..286

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA CGT AAC ACC AAC Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn	48
1 5 10 15	
CGC CGC CCC ATG GAC GTT AAG TTC CCG GGC GGT GGC CAG ATC GTT GGT Arg Arg Pro Met Asp Val Lys Phe Pro Gly Gly Gln Ile Val Gly	96
20 25 30	
GGA GTT TAC TTG TTG CCG CGC AGG GGC CCC AGG TTG GGT GTG CGC GCG Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala	144
35 40 45	
ACT AGG AAG ACT TCG GAG CGG TCG CAA CCT CGT GGG AGA CGT CAG CCT Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro	192
50 55 60	
ATC CCC AAG GCA CGT CGA TCT GAG GGA AGG TCC TGG GCT CAG CCC GGG Ile Pro Lys Ala Arg Arg Ser Glu Gly Arg Ser Trp Ala Gln Pro Gly	240
65 70 75 80	
TAC CCA TGG CCT CTT TAC GGT AAT GAG GGT TGT GGG TGG GCA GGA TGG G Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp	289
85 90 95	

(2) INFORMATION FOR SEQ ID NO: 192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn	
1 5 10 15	
Arg Arg Pro Met Asp Val Lys Phe Pro Gly Gly Gln Ile Val Gly	
20 25 30	
Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala	
35 40 45	
Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro	
50 55 60	
Ile Pro Lys Ala Arg Arg Ser Glu Gly Arg Ser Trp Ala Gln Pro Gly	

65	70	75	80
Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly		Trp Ala Gly Trp	
85	90	95	

(2) INFORMATION FOR SEQ ID NO: 193:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 498 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..498

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..495

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:

ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA CGT AAC ACC AAC Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn	48
1 5 10 15	
CGC CGC CCT ATG GAC GTA AAG TTC CCG GGC GGT GGA CAG ATC GTT GGC Arg Arg Pro Met Asp Val Lys Phe Pro Gly Gly Gln Ile Val Gly	96
20 25 30	
GGA GTT TAC TTG TTG CCG CGC AGG GGC CCC CGG TTG GGT GTG CGC GCG Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala	144
35 40 45	
ACT CGG AAG ACT TCG GAG CGG TCG CAA CCT CGT GGC AGG CGT CAA CCT Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro	192
50 55 60	
ATC CCC AAG GCG CGC CGG TCC GAG GGC AGG TCC TGG GCG CAA GCC GGG Ile Pro Lys Ala Arg Arg Ser Glu Gly Arg Ser Trp Ala Gln Ala Gly	240
65 70 75 80	
TAC CCC TGG CCC CTC TAT GGC AAT GAG GGC TGT GGG TGG GCA GGG TGG Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp	288
85 90 95	
CTC CTG TCT CCT CGC GGC TCT CGG CCA TCT TGG GGC CCA AAT GAT CCC	336

Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro			
100	105	110	
CGG CGG AGA TCG CGC AAT CTG GGT AAG GTC ATC GAT ACC CTG ACG TGC		384	
Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys			
115	120	125	
Gly TTC GCC GAC CTC ATG GGA TAC ATC CCG CTC GTG GGC GCC CCC GTC		432	
Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala Pro Val			
130	135	140	
GGG GGC GTC GCC AGG GCC CTG GCG CAT GGC GTC AGG GCT GTG GAG GAC		480	
Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val Glu Asp			
145	150	155	160
GGG ATT AAC TAT CGA CAG		498	
Gly Ile Asn Tyr Arg Gln			
165			

(2) INFORMATION FOR SEQ ID NO: 194:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 166 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn			
1	5	10	15
Arg Arg Pro Met Asp Val Lys Phe Pro Gly Gly Gln Ile Val Gly			
20	25	30	
Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala			
35	40	45	
Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro			
50	55	60	
Ile Pro Lys Ala Arg Arg Ser Glu Gly Arg Ser Trp Ala Gln Ala Gly			
65	70	75	80
Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp			
85	90	95	
Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro			
100	105	110	
Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys			
115	120	125	
Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala Pro Val			
130	135	140	

Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val Glu Asp
 145 150 155 160

Gly Ile Asn Tyr Arg Gln
 165

(2) INFORMATION FOR SEQ ID NO: 195:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 579 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 1..579

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
 (B) LOCATION: 1..576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

ACG TGC GGA TTC GCC GAC CTC GTG GGG TAC ATC CCG CTC GTA GGC GGC	48
Thr Cys Gly Phe Ala Asp Leu Val Gly Tyr Ile Pro Leu Val Gly Gly	
1 5 10 15	
CCC GTT GGG GGC GTC GCA AGG GCT CTC GCA CAT GGT GTG AGG GTT CTT	96
Pro Val Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu	
20 25 30	
GAG GAC GGG GTG AAT TAT GCA ACA GGG AAT CTG CCT GGT TGC TCT TTC	144
Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe	
35 40 45	
TCT ATC TTC ATT CTT GCA CTT CTC TCG TGC CTC ACT GTC CCG GCC TCT	192
Ser Ile Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser	
50 55 60	
GCA GTT CCC TAC CGA AAT GCC TCT GGG ATC TAT CAT GTC ACC AAT GAT	240
Ala Val Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp	
65 70 75 80	
TGC CCA AAC TCT TCC ATA GTC TAT GAG GCA GAT GAT CTG ATC CTA CAC	288
Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Leu Ile Leu His	
85 90 95	
GCA CCT GGC TGC GTG CCT TGT GTC AGG AAA GAT AAT GTG AGT AGG TGC	336

Ala Pro Gly Cys Val Pro Cys Val Arg Lys Asp Asn Val Ser Arg Cys		
100	105	110
TGG GTC CAA ATT ACC CCC ACG CTG TCA GCC CCG AGC TTC GGA GCA GTC		384
Trp Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Phe Gly Ala Val		
115	120	125
ACG GCT CCC CTT CGG AGA GCC GTT GAT TAC TTG GTG GGA GGG GCT GCC		432
Thr Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Val Gly Gly Ala Ala		
130	135	140
CTC TGC TCC GCG TTA TAC GTT GGA GAC GCG TGT GGG GCA CTA TTT TTG		480
Leu Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe Leu		
145	150	155
GTA GGC CAA ATG TTC ACC TAT AGG CCT CGC CAG CAT GCT ACG GTG CAG		528
Val Gly Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val Gln		
165	170	175
GAC TGC AAC TGT TCC ATC TAC AGT GGC CAC GTC ACC GGC CAT CAG ATG		576
Asp Cys Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Gln Met		
180	185	190
GCA		579
Ala		

(2) INFORMATION FOR SEQ ID NO: 196:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 193 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196:

Thr Cys Gly Phe Ala Asp Leu Val Gly Tyr Ile Pro Leu Val Gly Gly			
1	5	10	15
Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu			
20	25	30	
Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe			
35	40	45	
Ser Ile Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser			
50	55	60	
Ala Val Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp			
65	70	75	80
Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Leu Ile Leu His			
85	90	95	
Ala Pro Gly Cys Val Pro Cys Val Arg Lys Asp Asn Val Ser Arg Cys			
100	105	110	

Trp Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Phe Gly Ala Val
 115 120 125

Thr Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Val Gly Gly Ala Ala
 130 135 140

Leu Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe Leu
 145 150 155 160

Val Gly Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val Gln
 165 170 175

Asp Cys Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Gln Met
 180 185 190

Ala

(2) INFORMATION FOR SEQ ID NO: 197:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 579 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..579

(x) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:

ACT TGC GGC TTT GCC GAC CTC ATG GGA TAC ATC CCG CTC GTA GGC GCC
 1 5 10

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala
 15

48

CCC GTG GGT GGC GTC GCC AGA GCC CTG GAA CAT GGT GTT AGG GCT GTG
 20 25 30

Pro Val Gly Val Ala Arg Ala Leu Glu His Gly Val Arg Ala Val

96

GAG GAC GGC ATC AAT TAT GCA ACA GGG AAT CTC CCC GGT TGC TCT TTC
 35 40 45

Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe

144

TCT ATC TAC CTC TTG GCA CTT CTC TCG TGC CTG ACT GTT CCC ACC TCG

192

Ser Ile Tyr Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Thr Ser			
50	55	60	
GCC ATC CAC TAT CGC AAT GCC TCG GGC GTC TAC CAC GTC ACC AAT GAC			240
Ala Ile His Tyr Arg Asn Ala Ser Gly Val Tyr His Val Thr Asn Asp			
65	70	75	80
TGC CCG AAC TCG AGC ATA GTG TAC GRG GAC CAC CAC ATC CTA CAC			288
Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Leu His			
85	90	95	
CTT CCA GGG TGC TTA CCC TGT GTG AGG GTT GGG AAT CAG TCA CGT TGT			336
Leu Pro Gly Cys Leu Pro Cys Val Arg Val Gly Asn Gln Ser Arg Cys			
100	105	110	
TGG GTG GCC CTC TCT CCC ACC GTG GCG GCG CCT TAC ATC GGT GCT CCA			384
Trp Val Ala Leu Ser Pro Thr Val Ala Ala Pro Tyr Ile Gly Ala Pro			
115	120	125	
GTT GAA TCC TTC CGG AGA CAC GTG GAC ATG ATG GTG GGC GCT GCT ACT			432
Val Glu Ser Phe Arg Arg His Val Asp Met Met Val Gly Ala Ala Thr			
130	135	140	
GTG TGC TCC GCT CTC TAT ATT GGG GAC TTG TGT GGT GGC GTA TTC TTG			480
Val Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu			
145	150	155	160
GTT GGT CAG ATG TTT TCT TTC CGG CCA CGA CGC CAC TGG ACT ACG CAG			528
Val Gly Gln Met Phe Ser Phe Arg Pro Arg Arg His Trp Thr Thr Gln			
165	170	175	
GAC TGC AAT TGT TCC ATC TAC GCG GGG CAC ATC ACT GGC CAC GGA ATG			576
Asp Cys Asn Cys Ser Ile Tyr Ala Gly His Ile Thr Gly His Gly Met			
180	185	190	
GCA			579
Ala			

(2) INFORMATION FOR SEQ ID NO: 198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala			
1	5	10	15
Pro Val Gly Gly Val Ala Arg Ala Leu Glu His Gly Val Arg Ala Val			
20	25	30	
Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe			

35 40 45

Ser Ile Tyr Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Thr Ser
50 55 60

Ala Ile His Tyr Arg Asn Ala Ser Gly Val Tyr His Val Thr Asn Asp
65 70 75 80

Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Leu His
85 90 95

Leu Pro Gly Cys Leu Pro Cys Val Arg Val Gly Asn Gln Ser Arg Cys
100 105 110

Trp Val Ala Leu Ser Pro Thr Val Ala Ala Pro Tyr Ile Gly Ala Pro
115 120 125

Val Glu Ser Phe Arg Arg His Val Asp Met Met Val Gly Ala Ala Thr
130 135 140

Val Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu
145 150 155 160

Val Gly Gln Met Phe Ser Phe Arg Pro Arg Arg His Trp Thr Thr Gln
165 170 175

Asp Cys Asn Cys Ser Ile Tyr Ala Gly His Ile Thr Gly His Gly Met
180 185 190

Ala

(2) INFORMATION FOR SEQ ID NO: 199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1470 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..1470

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 2..1467

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199:

A TCA CCA CCG GAG CTT CTA TCA CAT ACT CCA CTT ACG GCA AGT TCC Ser Pro Pro Glu Leu Leu Ser His Thr Pro Leu Thr Ala Ser Ser 1 5 10 15	46
TTG CTG ATG GAG GGT GTT CAG GCG CGC ATG ACG TGA TCA TAT GCG Leu Leu Met Glu Gly Val Gln Ala Ala Arg Met Thr * Ser Tyr Ala 20 25 30	94
ACG AGT GCC ATT CCC AGG ACG CCA CCA TTC TTG GGA TAG GCA CTG Thr Ser Ala Ile Pro Arg Thr Pro Pro Phe Leu Gly * Ala Leu 35 40 45	142
TCC TTG ACC AGG CAG AGA CGG CTG GAG CTA GGC TCG TCG TCT TGG CCA Ser Leu Thr Arg Gln Arg Arg Leu Glu Leu Gly Ser Ser Ser Trp Pro 50 55 60	190
CGG CCA CCC CTC CCG GCA GTG TGA CAA CGC CCC ACC CCA ACA TCG AGG Arg Pro Pro Leu Pro Ala Val * Gln Arg Pro Thr Pro Thr Ser Arg 65 70 75	238
AAG TGG CCC TGC CTC AGG AGG GGG AGG TTC CCT TCT ACG GCA GAG CCA Lys Trp Pro Cys Leu Arg Arg Gly Arg Phe Pro Ser Thr Ala Glu Pro 80 85 90 95	286
TTC CCC TTG CTT TTA TAA AGG GTG GTA GGC ATC TCA TCT TCT GCC ATT Phe Pro Leu Leu Leu * Arg Val Val Gly Ile Ser Ser Ser Ala Ile 100 105 110	334
CCA AGA AAA AAT GTG ATG AAC TCG CCA AGC AAC TGA CCA GCC TGG GCG Pro Arg Lys Asn Val Met Asn Ser Pro Ser Asn * Pro Ala Trp Ala 115 120 125	382
TGA ACG CCG TGG CAT ATT ATA GAG GTC TAG ACG TCG CCG TCA TAC CCA * Thr Pro Trp His Ile Ile Glu Val * Thr Ser Pro Ser Tyr Pro 130 135 140	430
CAA CAG GAG ACG TGG TCG TGT GCA GCA CCG ACG CGC TCA TGA CGG GAT Gln Gln Glu Thr Trp Ser Cys Ala Ala Pro Thr Arg Ser * Arg Asp 145 150 155	478
TCA CCG GCG ACT TTG ATT CTG TCA TAG ACT GCA ACT CCG CCG TCA CTC Ser Pro Ala Thr Leu Ile Leu Ser * Thr Ala Thr Pro Pro Ser Leu 160 165 170 175	526
AGA CGG TGG ACT TCA GTC TGG ATC CCA CTT TTA CCA TTG AGA CTA CCA Arg Arg Trp Thr Ser Val Trp Ile Pro Leu Leu Pro Leu Arg Leu Pro 180 185 190	574
CAG TGC CCC AGG ACG CAG TGT CCA GAA GCC AGC GTT GGG GCC GCA CGG Gln Cys Pro Arg Thr Gln Cys Pro Glu Ala Ser Val Gly Ala Ala Arg 195 200 205	622
GGA GAG GTA GGC ACG GCA TAT ACC GGT ATG TCT CGG CTG GAG AGA GAC Gly Glu Val Gly Thr Ala Tyr Thr Gly Met Ser Arg Leu Glu Arg Asp 210 215 220	670
CGT CTG GCA TGT TCG ACT CCG TGG TGC TCT GTG AGT GCT ACG ATG CCG Arg Leu Ala Cys Ser Thr Pro Trp Cys Ser Val Ser Ala Thr Met Pro	718

225	230	235	
GAT GTG CAT GGT ACG ATC TGA CTC CTG CCG AGA CTA CCG TGA GGT TGC Asp Val His Gly Thr Ile * Leu Leu Pro Arg Leu Pro * Gly Cys 240 245 250 255			766
GCG CTT ACT AAA CAC CCC CGG GCT CCC TGT CTG TCA GGA CCA TTT GGA Ala Leu Thr Lys His Pro Arg Ala Pro Cys Leu Ser Gly Pro Phe Gly 260 265 270			814
ATT CTG GGA GGG GGT GTT CAC GGG GCT CAC TAA CAT CGA CGC TCA CAT Ile Leu Gly Gly Val His Gly Ala His * His Arg Arg Ser His 275 280 285			862
GCT GTC ACA GAC CAA ACA GGG TGG GGA GAA TTT CCC ATA CCT TGT AGC Ala Val Thr Asp Gln Thr Gly Trp Gly Glu Phe Pro Ile Pro Cys Ser 290 295 300			910
GTA CCA AGC AAC AGT CTG TGT TCG CGC GAA AGC GCC CCC CAG CTG Val Pro Ser Asn Ser Leu Cys Ser Arg Glu Ser Ala Pro Pro Gln Leu 305 310 315			958
GGA CAC AAT GTG GAA ATG CAT GCT CCG TCT CAA ACC GAC TTA ACT GGC Gly His Asn Val Glu Met His Ala Pro Ser Gln Thr Asp Leu Thr Gly 320 325 330 335			1006
CCT ACT CCC CTC TTG TAC AGG CTG GGG CCC GTC CAG AAT GAG ATC ACA Pro Thr Pro Leu Leu Tyr Arg Leu Gly Pro Val Gln Asn Glu Ile Thr 340 345 350			1054
CTG ACG CAC CCC ATC ACC AAG TAC ATT ATG GCT TGC ATG TCT GCG GAC Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met Ser Ala Asp 355 360 365			1102
TTG GAG GTC ATT ACC AGC ACT TGG GTT CTG GTG GGG GGC GTT GTG GCG Leu Glu Val Ile Thr Ser Thr Trp Val Leu Val Gly Gly Val Val Ala 370 375 380			1150
GCC CTG GCG GCC TAC TGC TTG ACG GTG GGT TCG GTA GCC ATA GTC GGT Ala Leu Ala Ala Tyr Cys Leu Thr Val Gly Ser Val Ala Ile Val Gly 385 390 395			1198
AGG ATC ATC CTC TCT GGG AAA CCT GCC ATC ATT CCC GAT AGG GAG GTA Arg Ile Ile Leu Ser Gly Lys Pro Ala Ile Ile Pro Asp Arg Glu Val 400 405 410 415			1246
TTA TAC CAG CAA TTT GAT GAG ATG GAG GAG TGC TCG GCC TCG TTG CCC Leu Tyr Gln Gln Phe Asp Glu Met Glu Glu Cys Ser Ala Ser Leu Pro 420 425 430			1294
TAT ATG GAC GAA ACA CGT GCC ATT GCC GGA CAA TTC AAA GAG AAA GTG Tyr Met Asp Glu Thr Arg Ala Ile Ala Gly Gln Phe Lys Glu Lys Val 435 440 445			1342
CTC GGC TTC ATC AGC ACG ACC GGC CAG AAG GCT GAA ACT CTG AAG CCG Leu Gly Phe Ile Ser Thr Thr Gly Gln Lys Ala Glu Thr Leu Lys Pro 450 455 460			1390

GCA GCC ACG TCT GTG TGG AAC AAG GCT GAG CAG TTC TGG CCA CAT ACA Ala Ala Thr Ser Val Trp Asn Lys Ala Glu Gln Phe Trp Pro His Thr	1438
465 470 475	

TGT GGA ACT TCA TCA GTG GGA TAC AAT AAT AG Cys Gly Thr Ser Ser Val Gly Tyr Asn Asn	1470
480 485	

(2) INFORMATION FOR SEQ ID NO: 197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1485 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1485

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:

TGTGCCAGGA CCATCACCAAC CGGAGCTTCT ATCACCTACT CCACCTACGG CAAGTTCCCTT	60
GCTGATGGAG GGTGTTCAAGG CGGGCGCGAT GACGTGATCA TATGCCACGA GTGCCATTCC	120
CAGGACGCCA CCACCATTCT TGGGATAGGC ACTGTCTTGT ACCAGGGCAGA GACGGCTGGAA	180
GCTAGGCTCG TCGTCTTGGC CACGGCCACC CCTCCGGCA GTGTGACAAC GCCCCACCCCC	240
AACATCGAGG AAGTGGCCCT GCCTCAGGAG GGGGAGGGTTC CCTTCTACGG CAGAGCCATT	300
CCCCTTGCTT TTATAAAGGG TGGTAGGCAT CTCATCTTCT GCCATTCCAA GAAAAAAATGT	360
GATGAACTCG CCAAGCAACT GACCAGCCTG GGCGTGAACG CCGTGGCATA TTATAGAGGT	420
CTAGACGTCG CCGTCATACC CACAACAGGA GACGTGGTCG TGTGCAGCAC CGACGCGCTC	480
ATGACGGGAT TCACCGGCCGA CTTTGATTCT GTCATAGACT GCAACTCCGC CGTCACTCAG	540
ACGGTGGACT TCAGTCTGGA TCCCACTTTT ACCATTGAGA CTACCACAGT GCCCCAGGAC	600
GCAGTGTCCA GAAGCCAGCG TTGGGGCCGC ACGGGGAGAG GTAGGCACGG CATATAACCGG	660
TATGTCTCGG CTGGAGAGAG ACCGTCTGGC ATGTTGACT CCGTGGTGCT CTGTGAGTGC	720
TACGATGCCG GATGTGCATG GTACGATCTG ACTCCTGCCG AGACTACCCT GAGGTTGCC	780
GCTTACNTAA ACACCCCCGG GCTCCCTGTC TGTCAGGACC ATTTGGAATT CTGGGAGGGG	840
GTGTTCACGG GGCTCACTAA CATCGACGCT CACATGCTGT CACAGACCAA ACAGGGTGGG	900
GAGAATTTCCTACACCTTGT AGCGTACCAA GCAACAGTCT GTGTTGCCGC GAAAGCGCCC	960

CCCCCCCAGCT	GGGACACAAT	GTGGAAATGC	ATGCTCCGTC	TCAAACCGAC	NTTAACTGGC	1020
CCTACTCCCC	TCTTGTACAG	GCTGGGGCCC	GTCCAGAACG	AGATCACACT	GACGCACCCC	1080
ATCACCAAGT	ACATTATGGC	TTGCATGTCT	GCGGACTTGG	AGGTCAATTAC	CAGCACTTGG	1140
GTTCTGGTGG	GGGGCGTTGT	GGCGGCCCTG	GCGGCCTACT	GCTTGACGGT	GGGTTCGGTA	1200
GCCATAGTCG	GTAAGGATCAT	CCTCTCTGGG	AAACCTGCCA	TCATTCCGA	TAGGGAGGTA	1260
TTATACCAGC	AATTTGATGA	GATGGAGGAG	TGCTCGGCCT	CGTTGCCCTA	TATGGACGAA	1320
ACACGTGCCA	TTGCCGGACA	ATTCAAAGAG	AAAGTGCTCG	GCTTCATCAG	CACGACCGGC	1380
CAGAAGGCTG	AAACTCTGAA	GCCGGCAGCC	ACGTCTGTGT	GGAAACAAGGC	TGAGCAGTTC	1440
TGGNCCACAT	ACATGTGGAA	CTTCATCAAGT	GGGATAACAAT	AATAG		1485

(2) INFORMATION FOR SEQ ID NO: 198:

- (i) SEQUENCE CHARACTERISTICS.
 - (A) LENGTH: 484 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198:

Cys	Ala	Arg	Thr	Ile	Thr	Thr	Gly	Ala	Ser	Ile	Thr	Tyr	Ser	Thr	Tyr
1					5					10				15	
Gly	Lys	Phe	Leu	Ala	Asp	Gly	Gly	Cys	Ser	Gly	Gly	Ala	His	Asp	Val
					20				25				30		
Ile	Ile	Cys	Asp	Glu	Cys	His	Ser	Gln	Asp	Ala	Thr	Thr	Ile	Leu	Gly
						35		40				45			
Ile	Gly	Thr	Val	Leu	Asp	Gln	Ala	Glu	Thr	Ala	Gly	Ala	Arg	Leu	Val
					50		55			60					
Val	Leu	Ala	Thr	Ala	Thr	Pro	Pro	Gly	Ser	Val	Thr	Thr	Pro	His	Pro
					65		70		75		80				
Asn	Ile	Glu	Glu	Val	Ala	Leu	Pro	Gln	Glu	Gly	Glu	Val	Pro	Phe	Tyr
					85		90				95				
Gly	Arg	Ala	Ile	Pro	Leu	Ala	Phe	Ile	Lys	Gly	Gly	Arg	His	Leu	Ile
					100		105				110				
Phe	Cys	His	Ser	Lys	Lys	Cys	Asp	Glu	Leu	Ala	Lys	Gln	Leu	Thr	
					115		120			125					
Ser	Leu	Gly	Val	Asn	Ala	Val	Ala	Tyr	Tyr	Arg	Gly	Leu	Asp	Val	Ala
					130		135			140					

Val Ile Pro Thr Thr Gly Asp Val Val Val Cys Ser Thr Asp Ala Leu
145 150 155 160

Met Thr Gly Phe Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn Ser
165 170 175

Ala Val Thr Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr Ile
180 185 190

Glu Thr Thr Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg Trp
195 200 205

Gly Arg Thr Gly Arg Gly Arg His Gly Ile Tyr Arg Tyr Val Ser Ala
210 215 220

Gly Glu Arg Pro Ser Gly Met Phe Asp Ser Val Val Leu Cys Glu Cys
225 230 235 240

Tyr Asp Ala Gly Cys Ala Trp Tyr Asp Leu Thr Pro Ala Glu Thr Thr
245 250 255

Val Arg Leu Arg Ala Tyr Xaa Asn Thr Pro Gly Leu Pro Val Cys Gln
260 265 270

Asp His Leu Glu Phe Trp Glu Gly Val Phe Thr Gly Leu Thr Asn Ile
275 280 285

Asp Ala His Met Leu Ser Gln Thr Lys Gln Gly Gly Glu Asn Phe Pro
290 295 300

Tyr Leu Val Ala Tyr Gln Ala Thr Val Cys Val Arg Ala Lys Ala Pro
305 310 315 320

Pro Pro Ser Trp Asp Thr Met Trp Lys Cys Met Leu Arg Leu Lys Pro
325 330 335

Xaa Leu Thr Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Pro Val Gln
340 345 350

Asn Glu Ile Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys
355 360 365

Met Ser Ala Asp Leu Glu Val Ile Thr Ser Thr Trp Val Leu Val Gly
370 375 380

Gly Val Val Ala Ala Leu Ala Ala Tyr Cys Leu Thr Val Gly Ser Val
385 390 395 400

Ala Ile Val Gly Arg Ile Ile Leu Ser Gly Lys Pro Ala Ile Ile Pro
405 410 415

Asp Arg Glu Val Leu Tyr Gln Gln Phe Asp Glu Met Glu Glu Cys Ser
420 425 430

Ala Ser Leu Pro Tyr Met Asp Glu Thr Arg Ala Ile Ala Gly Gln Phe
435 440 445

Lys Glu Lys Val Leu Gly Phe Ile Ser Thr Thr Gly Gln Lys Ala Glu
 450 455 460

Thr Leu Lys Pro Ala Ala Thr Ser Val Trp Asn Lys Ala Glu Gln Phe
 465 470 475 480

Trp Xaa Thr Tyr

(2) INFORMATION FOR SEQ ID NO: 199:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1485 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 1..1485

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199:

TGTGCCAGGA CCATCACCCAC CGGAGCTTCT ATCACATACT CCACTTACGG CAAGTTCCCTT 60
GCTGATGGAG GGTGTTCAAG CGGCAGCGTAT GACGTGATCA TATGCGACGA GTGCCATTCC 120
CAGGACGCCA CCACCATTCT TGGGATAGGC ACTGTCCTTG ACCAGGCAGA GACGGCTGGA 180
GCTAGGCTCG TCGTCTTGGC CACGGCCACC CCTCCCGGCA GTGTGACAAC GCCCCACCCC 240
AACATCGAGG AAGTGGCCCT GCCTCAGGAG GGGGAGGTTTC CCTTCTACGG CAGAGCCATT 300
CCCCTTGCTT TTATAAAGGG TGGTAGGCAT CTCATCTTCT GCCATTCCAA GAAAAAAATGT 360
GATGAACTCG CCAAGCAACT GACCAGCCTG GGCGTGAACG CCGTGGCATA TTATAGAGGT 420
CTAGACGTCTG CCGTCATCCC CACAGCAGGA GACGTGGCTG TGTGCAGCAC CGACGCGCTC 480
ATGACGGGAT TCACCGCGA CTTTGATTCT GTCATAGACT GCAACTCCGC CGTCACTCAG 540
ACGGTGGACT TCAGTCTGGA TCCCCACTTTT ACCATTGAGA CTACCACAGT GCCCCAGGAC 600
GCAGTGTCCA GAAGCCAGCG TAGGGGCCGC ACAGGGAGAG GTAGGCACGG CATATACCGG 660
TATGTCTCGG CTGGAGAGAG ACCNTCTGAC ATGTTCGACT CCGTGGTGCT CTGTGAGTGC 720
TACGATGCCG GATGTGCGTG GTATGATCTG ACTCCTGCCG AGACTACCGT GAGGTTGCGC 780
GCTTACATAA ACACCCCCGG GCTCCCTGTC TGTCAGGACC ATTTGGAATT CTGGGAGGGG 840
GTGTTCACGG GGCTCACTAA CATCGACGCT CACATGCTGT CACAGACCAA ACAGGGTGGG 900
GAGAATTTC CATACTTGT AGCGTACCAAC GCAACAGTCT GTGTTCGCGC GAAAGCGCCC 960

CCCCCCAGCT	GGGACACAAT	GTGGAAATGC	ATGCTCCGTC	TCAAACCGAC	TTAACTGGC	1020
CCTACTCCCC	TCTTGTACAG	GCTGGGGCCC	GTCCAGANTG	AGATCACACT	GACGCACCCC	1080
ATCACCAAGT	ACATTATGGC	TTGCATGTCT	GCGGACTTGG	AGGTCAATTAC	CANCACTTGG	1140
GTTCCTGGTGG	GGGGCGTTGT	GGCGGCCCTG	GCGGCCTACT	GCTTGACGGT	GGGTTCGGTA	1200
GCCATAGTCG	GTAGGATCAT	CCTCTCTGGG	AAACCTGCCA	TCATTCCGA	TAGGGAGGCA	1260
TTATACCAGC	AATTTGATGA	GATGGAGGAG	TGCTCGGCCT	C3TTGCCCTA	TATGGACGAG	1320
ACACGTGCCA	TTGCCGGACA	ATTCAAAGAG	AAAGTGCTCG	GCTTCATCAG	CACGACCGGC	1380
CAGAAGGCTG	AAACTCTGAA	GCCGGCAGCC	ACGTCTGTGT	GGAACAAGGC	TGAGCAGTTC	1440
TGGGCCACAT	ACATGTGGAA	CTTCATCAGC	GGGATACAAT	AATAG		1485

(2) INFORMATION FOR SEQ ID NO: 200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 484 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200:

Cys	Ala	Arg	Thr	Ile	Thr	Thr	Gly	Ala	Ser	Ile	Thr	Tyr	Ser	Thr	Tyr
1				5						10				15	

Gly	Lys	Phe	Leu	Ala	Asp	Gly	Gly	Cys	Ser	Gly	Gly	Ala	Tyr	Asp	Val
						20			25				30		

Ile	Ile	Cys	Asp	Glu	Cys	His	Ser	Gln	Asp	Ala	Thr	Thr	Ile	Leu	Gly
						35			40				45		

Ile	Gly	Thr	Val	Leu	Asp	Gln	Ala	Glu	Thr	Ala	Gly	Ala	Arg	Leu	Val
						50			55				60		

Val	Leu	Ala	Thr	Ala	Thr	Pro	Pro	Gly	Ser	Val	Thr	Thr	Pro.	His	Pro
65						70			75				80		

Asn	Ile	Glu	Glu	Val	Ala	Leu	Pro	Gln	Glu	Gly	Glu	Val	Pro	Phe	Tyr
							85			90			95		

Gly	Arg	Ala	Ile	Pro	Leu	Ala	Phe	Ile	Lys	Gly	Gly	Arg	His	Leu	Ile
							100		105				110		

Phe	Cys	His	Ser	Lys	Lys	Cys	Asp	Glu	Leu	Ala	Lys	Gln	Leu	Thr	
							115		120				125		

Ser Leu Gly Val Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val Ala
 130 135 140
 Val Ile Pro Thr Ala Gly Asp Val Val Cys Ser Thr Asp Ala Leu
 145 150 155 160
 Met Thr Gly Phe Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn Ser
 165 170 175
 Ala Val Thr Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr Ile
 180 185 190
 Glu Thr Thr Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg Arg
 195 200 205
 Gly Arg Thr Gly Arg Gly His Gly Ile Tyr Arg Tyr Val Ser Ala
 210 215 220
 Gly Glu Arg Xaa Ser Asp Met Phe Asp Ser Val Val Leu Cys Glu Cys
 225 230 235 240
 Tyr Asp Ala Gly Cys Ala Trp Tyr Asp Leu Thr Pro Ala Glu Thr Thr
 245 250 255
 Val Arg Leu Arg Ala Tyr Ile Asn Thr Pro Gly Leu Pro Val Cys Gln
 260 265 270
 Asp His Leu Glu Phe Trp Glu Gly Val Phe Thr Gly Leu Thr Asn Ile
 275 280 285
 Asp Ala His Met Leu Ser Gln Thr Lys Gln Gly Glu Asn Xaa Pro
 290 295 300
 Tyr Leu Val Ala Tyr Gln Ala Thr Val Cys Val Arg Ala Lys Ala Pro
 305 310 315 320
 Pro Pro Ser Trp Asp Thr Met Trp Lys Cys Met Leu Arg Leu Lys Pro
 325 330 335
 Thr Leu Thr Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Pro Val Gln
 340 345 350
 Xaa Glu Ile Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys
 355 360 365
 Met Ser Ala Asp Leu Glu Val Ile Thr Xaa Thr Trp Val Leu Val Gly
 370 375 380
 Gly Val Val Ala Ala Leu Ala Ala Tyr Cys Leu Thr Val Gly Ser Val
 385 390 395 400
 Ala Ile Val Gly Arg Ile Ile Leu Ser Gly Lys Pro Ala Ile Ile Pro
 405 410 415
 Asp Arg Glu Ala Leu Tyr Gln Gln Phe Asp Glu Met Glu Glu Cys Ser
 420 425 430
 Ala Ser Leu Pro Tyr Met Asp Glu Thr Arg Ala Ile Ala Gly Gln Phe

435

440

445

Lys Glu Lys Val Leu Gly Phe Ile Ser Thr Thr Gly Gln Lys Ala Glu
 450 455 460

Thr Leu Lys Pro Ala Ala Thr Ser Val Trp Asn Lys Ala Glu Gln Phe
 465 470 475 480

Trp Ala Thr Tyr

(2) INFORMATION FOR SEQ ID NO: 201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..340

(x) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 2..337

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:

C TCC ACT GTG ACT GAG AGA GAC ATC AGG GTC GAA GAA GAA GTC TAT	46
Ser Thr Val Thr Glu Arg Asp Ile Arg Val Glu Glu Val Tyr	
1 5 10 15	
CAG TGT TGT GAT CTG GAG CCC GAG GCC CGC AAG GTA ATA ACC GCC CTC	94
Gln Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Thr Ala Leu	
20 25 30	
ACG GAG AGA CTC TAC GTG GGC GGC CCT ATG TAC AAT AGC AAG GGA GAC	142
Thr Glu Arg Leu Tyr Val Gly Gly Pro Met Tyr Asn Ser Lys Gly Asp	
35 40 45	
CTT TGC GGG TAT CGC AGG TGC CGC GCA AGC GGC GTA TAT ACC ACC AGC	190
Leu Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Ser	
50 55 60	
TTC GGG AAC ACA CTG ACG TGC TAC CTT AAA GCC TCA GCA GCC ATC AGG	238
Phe Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Ile Arg	
65 70 75	
GCT GCG GGG CTG AAG GAC TGC ACC ATG CTG GTT TGC GGT GAC GAC TTA	286
Ala Ala Gly Leu Lys Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu	
80 85 90 95	

GTC GTG ATC GCT GAA AGC GGT GCC GTC GAG GAG GAC AAG CGA GCC CTC 334
 Val Val Ile Ala Glu Ser Gly Gly Val Glu Glu Asp Lys Arg Ala Leu
 100 105 110

GGA GCT
Gly Ala 340

(2) INFORMATION FOR SEQ ID NO: 202:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(i) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202:

Ser	Thr	Val	Thr	Glu	Arg	Asp	Ile	Arg	Val	Glu	Glu	Glu	Val	Tyr	Gln
1									10					15	
Cys	Cys	Asp	Leu	Glu	Pro	Glu	Ala	Arg	Lys	Val	Ile	Thr	Ala	Leu	Thr
20									25					30	

Glu Arg Leu Tyr Val Gly Gly Pro Met Tyr Asn Ser Lys Gly Asp Leu
35 40 45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser Phe
 50 55 60

Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Ile Arg Ala
65 70 75 80

Ala Gly Leu Lys Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val
85 90 95

Val Ile Ala Glu Ser Gly Gly Val Glu Glu Asp Lys Arg Ala Leu Gly
100 105 110

Ala **Asp** **Cys** **Glu** **Ile** **Lys** **Leu** **Met** **Phe** **Pro** **Val**

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(2) INFORMATION FOR SEQ ID NO: 205.

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 340 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

iii) HYPOTHETICAL: NO

iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..340

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 2..337

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

C TCC ACA GTG ACT GAR AGA GAC ATC AGG GTC GAG GAA GAG GTC TAC	46
Ser Thr Val Thr Glu Arg Asp Ile Arg Val Glu Glu Val Tyr	
1 5 10 15	
CAG TGT TGT GAC CTG GAG CCT GAA ACC CGC AAG GTA ATA TCT GCC CTC	94
Gln Cys Cys Asp Leu Glu Pro Glu Thr Arg Lys Val Ile Ser Ala Leu	
20 25 30	
ACT GAA AGA CTC TAT GTG GGC GGT CCC ATG SAC AAC AGC AGG GGA GAC	142
Thr Glu Arg Leu Tyr Val Gly Gly Pro Met His Asn Ser Arg Gly Asp	
35 40 45	
CTA TGC GGG TAC CGT AGA TGC CGC GCG AGC GGC GTA TAC ACC ACA AGC	190
Leu Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser	
50 55 60	
TTC GGG AAC ACT CTG ACG TGC TTC CTC AAG GCC ACA GCG GCC ACC AAA	238
Phe Gly Asn Thr Leu Thr Cys Phe Leu Lys Ala Thr Ala Ala Thr Lys	
65 70 75	
GCC GCT GGC CTA AAG GAC TGC ACC ATG TTG GTG TGT GGT GAC GAC TTA	286
Ala Ala Gly Leu Lys Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu	
80 85 90 95	
GTC GTT ATC GCC GAA AGC GAT GGT GTC GAA GAG GAC CGC CGA GCC CTC	334
Val Val Ile Ala Glu Ser Asp Gly Val Glu Glu Asp Arg Arg Ala Leu	
100 105 110	
GGA GCT	340
Gly Ala	

(2) INFORMATION FOR SEQ ID NO: 204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204:

Ser Thr Val Thr Glu Arg Asp Ile Arg Val Glu Glu Glu Val Tyr Gln	
1 5 10 15	

Cys Cys Asp Leu Glu Pro Glu Thr Arg Lys Val Ile Ser Ala Leu Thr
 20 25 30

Glu Arg Leu Tyr Val Gly Gly Pro Met His Asn Ser Arg Gly Asp Leu
 35 40 45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser Phe
 50 55 60

Gly Asn Thr Leu Thr Cys Phe Leu Lys Ala Thr Ala Ala Thr Lys Ala
 65 70 75 80

Ala Gly Leu Lys Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val
 85 90 95

Val Ile Ala Glu Ser Asp Gly Val Glu Glu Asp Arg Arg Ala Leu Gly
 100 105 110

Ala

(2) INFORMATION FOR SEQ ID NO: 205:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 340 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..340

- (ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 2..337

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

C TCC ACG GTG ACC GAA AGG GAT ATC AGG ACC GAG GAA GAG ATC TAC	46
Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Glu Ile Tyr	
1 5 10 15	
CAG TGC TGC GAC CTG GAG CCC GAA GCC CGC AAG GTG ATA TCC GCC CTA	94
Gln Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Ser Ala Leu	
20 25 30	
ACG GAA AGA CTC TAC GTG GGC GGT CCC ATG TAC AAC TCC AAG GGG GAC	142
Thr Glu Arg Leu Tyr Val Gly Gly Pro Met Tyr Asn Ser Lys Gly Asp	
35 40 45	

CTA TGC GGG CAA CGG AGG TGC CGC GCA AGC GGG GTC TAC ACC ACC AGC	190		
Leu Cys Gly Gln Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser			
50	55	60	
TTC GGG AAC ACT GTA ACG TGT TAT CTC AAG GCC GTT GCG GCT ACT AGG	238		
Phe Gly Asn Thr Val Thr Cys Tyr Leu Lys Ala Val Ala Ala Thr Arg			
65	70	75	
GCC GCA GGT CTG AAA GGT TGC AGC ATG CTG GTT TGT GGA GAC GAC TTA	286		
Ala Ala Gly Leu Lys Gly Cys Ser Met Leu Val Cys Gly Asp Asp Leu			
80	85	90	95
GTC GTC ATC TGC GAG AGC GGC GGC GTA GAG GAG GAT GCA AGA GCC CTC	334		
Val Val Ile Cys Glu Ser Gly Gly Val Glu Glu Asp Ala Arg Ala Leu			
100	105	110	
CGA GCC			
Arg Ala			340

(2) INFORMATION FOR SEQ ID NO: 206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206:

Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Glu Glu Ile Tyr Gln
 1 5 10 15

Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Ser Ala Leu Thr
 20 25 30

Glu Arg Leu Tyr Val Gly Gly Pro Met Tyr Asn Ser Lys Gly Asp Leu
 35 40 45

Cys Gly Gln Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser Phe
 50 55 60

Gly Asn Thr Val Thr Cys Tyr Leu Lys Ala Val Ala Ala Thr Arg Ala
 65 70 75 80

Ala Gly Leu Lys Gly Cys Ser Met Leu Val Cys Gly Asp Asp Leu Val
 85 90 95

Val Ile Cys Glu Ser Gly Val Glu Glu Asp Ala Arg Ala Leu Arg
 100 105 110

Ala

(2) INFORMATION FOR SEQ ID NO: 207:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..340

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 2..337

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207:

C TCC ACG GTG ACT GAA AGG GAC ATT AGG GTC GAG GAA GAG ATC TAC	46
Ser Thr Val Thr Glu Arg Asp Ile Arg Val Glu Glu Ile Tyr	
1 5 10 15	
CAG TGC TGT GAC CTG GAG CCC GAG GCA CGC AAG GTG ATA TCC GCT CTC	94
Gln Cys Cys Asp Leu Glu Pro Ala Arg Lys Val Ile Ser Ala Leu	
20 25 30	
ACA GAA AGA CTC TAC AAG GGC CCC ATG TAT AAC AGC AAG GGG GAC	142
Thr Glu Arg Leu Tyr Lys Gly Gly Pro Met Tyr Asn Ser Lys Gly Asp	
35 40 45	
CTA TGC GGG CTT CGG AGG TGC CGC GCA AGC GGG GTA TAC ACC ACA AGC	190
Leu Cys Gly Leu Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Ser	
50 55 60	
TTC GGG AAC ACG GTG ACA TGC TAC CTT AAA GCC ACA GCA GCC ACC AGG	238
Phe Gly Asn Thr Val Thr Cys Tyr Leu Lys Ala Thr Ala Ala Thr Arg	
65 70 75	
GCT GCA GGG CTG AAA GAT TGC ACT ATG CTG GTA TGC GGT GAC GAC TTA	286
Ala Ala Gly Leu Lys Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu	
80 85 90 95	
GTC GTT ATT GCC GAA AGC GGT GGC GTG GAG GAG GAC GGC CGA GCC CTC	334
Val Val Ile Ala Glu Ser Gly Gly Val Glu Glu Asp Ala Arg Ala Leu	
100 105 110	
CGA GCC	340
Arg Ala	

(2) INFORMATION FOR SEQ ID NO: 208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 208:

Ser	Thr	Val	Thr	Glu	Arg	Asp	Ile	Arg	Val	Glu	Glu	Glu	Ile	Tyr	Gln
1															

Cys	Cys	Asp	Leu	Glu	Pro	Glu	Ala	Arg	Lys	Val	Ile	Ser	Ala	Leu	Thr

Glu	Arg	Leu	Tyr	Lys	Gly	Gly	Pro	Met	Tyr	Asn	Ser	Lys	Gly	Asp	Leu

Cys	Gly	Leu	Arg	Arg	Cys	Arg	Ala	Ser	Gly	Val	Tyr	Thr	Thr	Ser	Phe

Gly	Asn	Thr	Val	Thr	Cys	Tyr	Leu	Lys	Ala	Thr	Ala	Ala	Thr	Arg	Ala

Ala	Gly	Leu	Lys	Asp	Cys	Thr	Met	Leu	Val	Cys	Gly	Asp	Asp	Leu	Val

Val	Ile	Ala	Glu	Ser	Gly	Val	Glu	Glu	Asp	Ala	Arg	Ala	Leu	Arg

Ala

(2) INFORMATION FOR SEQ ID NO: 209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209:

CCCCACCGTG	ACNGAGAGGG	ACNTCAGGGT	CGAGGAAGAG	GTCTATCACT	GCTGTAATCT	60
GGAGNCCGAT	GNCCGCAAGG	TCATCACCGC	CCTCACAGAG	AGACTCTACG	TGGGCGGCC	120

TATGCACAAAC AGCAAGGGAG ACCTGTGTGG CATCCGTAGA TGCCGCGCGA GCGGGCTTTA	180
CACCAACGAGC TTGGAAACA CGCTGACTTG CTACCTCAA A GCCACAGCGG CCACCAGGGC	240
CGCGGGCTTG AAGGATTGCA CCATGCTGGT CTGCGGNGAC GACCTGGTTG TCATTGCTGA	300
GAGCATTGGC ATAGACGAGG ACAAGCAAGC CCTCCGACT	340

(2) INFORMATION FOR SEQ ID NO: 210:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO
 (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 210:

Pro Thr Val Thr Glu Arg Asp Xaa Arg Val Glu Glu Glu Val Tyr Gln			
1	5	10	15

Cys Cys Asn Leu Glu Xaa Asp Xaa Arg Lys Val Ile Asn Ala Leu Thr		
20	25	30

Glu Arg Leu Tyr Val Gly Gly Pro Met His Asn Ser Lys Gly Asp Leu		
35	40	45

Cys Gly Ile Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Ser Phe		
50	55	60

Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Thr Ala Ala Thr Arg Ala			
65	70	75	80

Ala Gly Leu Lys Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val		
85	90	95

Val Ile Ala Glu Ser Ile Gly Ile Asp Glu Asp Lys Gln Ala Leu Arg		
100	105	110

Thr

(2) INFORMATION FOR SEQ ID NO: 211:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 340 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211:

CTCGACTGTG	NCCGAGAGGG	ACATCAGGAC	AGAGGGAGAG	GTCTATCACT	GTTGCGACCT	60
GGAACCAGAA	GCCCCGAGG	TAATCACCGC	CCTCACTGAG	AGACTCTATG	TGGGCGGACC	120
CATGTTAAC	AGCAAGGGAG	ACCTGTGCGG	ACAACGCCGG	TGCCGCGCAA	GCGGCGTGTT	180
CACCACCAGC	TTCGGGAAACA	CACTGACGTC	CTACCTTAAA	GCCACAGCTG	CTACTAGAGC	240
AGCCGGCTTA	AAAGATTGCA	CCATGCTGGT	CTGCCGTGAC	GACTTAGTCG	TTATTTCCGA	300
GAGCGCCGGT	GTGGAGGAGG	ATCCCANAAC	CCNNCGACCN			340

(2) INFORMATION FOR SEQ ID NO: 212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 212:

Ser	Thr	Val	Xaa	Glu	Arg	Asp	Ile	Arg	Thr	Glu	Gly	Glu	Val	Tyr	Gln
1							5							10	15

Cys	Cys	Asp	Leu	Glu	Pro	Glu	Ala	Arg	Lys	Val	Ile	Thr	Ala	Leu	Thr
											20	25		30	

Glu	Arg	Leu	Tyr	Val	Gly	Gly	Pro	Met	Phe	Asn	Ser	Lys	Gly	Asp	Leu
											35	40	45		

Cys	Gly	Gln	Arg	Arg	Cys	Arg	Ala	Ser	Gly	Val	Phe	Thr	Thr	Ser	Phe
											50	55	60		

Gly	Asn	Thr	Leu	Thr	Cys	Tyr	Leu	Lys	Ala	Thr	Ala	Ala	Thr	Arg	Ala
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

65

70

75

80

Ala	Gly	Leu	Lys	Asp	Cys	Thr	Met	Leu	Val	Cys	Gly	Asp	Asp	Leu	Val
							85			90				95	

Val	Ile	Ser	Glu	Ser	Ala	Gly	Val	Glu	Glu	Asp	Pro	Xaa	Thr	Xaa	Arg
							100		105				110		

Pro

(2) INFORMATION FOR SEQ ID NO: 213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..340

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 2..337

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213:

C	TCA	ACA	GTC	ACC	GAG	AAC	GAC	ATC	CGT	GTT	GAG	GAG	TCA	ATT	TAC	46
	Ser	Thr	Val	Thr	Glu	Asn	Asp	Ile	Arg	Val	Glu	Glu	Ser	Ile	Tyr	
1			5					10					15			
CAA	TGT	TGT	GAC	TTG	GCC	CCC	GAG	GCC	AGA	CAG	GCC	ATA	AAG	TCG	CTC	94
	Gln	Cys	Cys	Asp	Leu	Ala	Pro	Glu	Ala	Arg	Gln	Ala	Ile	Lys	Ser	Leu
					20			25				30				
ACA	GAG	CGG	CTT	TAT	ATC	GGG	GGT	CCC	CTG	ACT	AAT	TCA	AAG	GGG	CAG	142
	Thr	Glu	Arg	Leu	Tyr	Ile	Gly	Gly	Pro	Leu	Thr	Asn	Ser	Lys	Gly	Gln
					35			40				45				
AAC	TGT	GGC	TAT	CGC	CGA	TGC	CGC	GCA	AGC	GGC	GTG	CTG	ACG	ACC	AGC	190
	Asn	Cys	Gly	Tyr	Arg	Arg	Cys	Arg	Ala	Ser	Gly	Val	Leu	Thr	Thr	Ser
					50			55				60				
TGC	GGT	AAT	ACC	CTT	ACA	TGT	TAC	CTA	AAG	GCC	TCT	GCA	GCC	TGT	CGA	238
	Cys	Gly	Asn	Thr	Leu	Thr	Cys	Tyr	Leu	Lys	Ala	Ser	Ala	Ala	Cys	Arg
					65			70			75					
GCT	GCG	AAG	CTC	CAG	GAC	TGC	ACG	ATG	CTC	GTG	TGC	GGG	GAC	GAC	CTT	286

Ala Ala Lys Leu Gln Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu	80	85	90	95
---	----	----	----	----

GTC GTT ATC TGT GAA AGC GCG GGA ACC CAA GAG GAC GCG GCG AGC CTA	334	
Val Val Ile Cys Glu Ser Ala Gly Thr Gln Glu Asp Ala Ala Ser Leu		
100	105	110

CGA GTC	340
Arg Val	

(2) INFORMATION FOR SEQ ID NO: 214:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 214:

Ser Thr Val Thr Glu Asn Asp Ile Arg Val Glu Glu Ser Ile Tyr Gln			
1	5	10	15

Cys Cys Asp Leu Ala Pro Glu Ala Arg Gln Ala Ile Lys Ser Leu Thr		
20	25	30

Glu Arg Leu Tyr Ile Gly Gly Pro Leu Thr Asn Ser Lys Gly Gln Asn		
35	40	45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Thr Thr Ser Cys		
50	55	60

Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Cys Arg Ala			
65	70	75	80

Ala Lys Leu Gln Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val		
85	90	95

Val Ile Cys Glu Ser Ala Gly Thr Gln Glu Asp Ala Ala Ser Leu Arg		
100	105	110

Val

(2) INFORMATION FOR SEQ ID NO: 215:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 340 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..340

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 2..340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215:

C TCA ACC GTC ACG GAG AGG GAT ATA AGA ACA GAA GAA TCC ATA TAT Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Glu Ser Ile Tyr	46
1 5 10 15	
CAA GCT TGT TCC CTG CCC CAA GAG GCC AGA ACT GTC ATA CAC TCG CTC Gln Ala Cys Ser Leu Pro Gln Glu Ala Arg Thr Val Ile His Ser Leu	94
20 25 30	
ACC GAG AGA CTC TAC GTG GGA GGG CCC ATG ATA AAC AGC AAA GGG CAA Thr Glu Arg Leu Tyr Val Gly Gly Pro Met Ile Asn Ser Lys Gly Gln	142
35 40 45	
TCC TGC GGT TAC AGG CGT TGC CGC GCA AGC GGT GTT TTC ACC ACC AGC Ser Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser	190
50 55 60	
ATG GGG AAT ACC ATG ACG TGT TAC ATC AAA GCC CTT GCA GCG TGT AAA Met Gly Asn Thr Met Thr Cys Tyr Ile Lys Ala Leu Ala Ala Cys Lys	238
65 70 75	
GCC GCA GGG ATC GTG GAC CCC GTC ATG CTG GTG TGT GGA GAC GAC CTG Ala Ala Gly Ile Val Asp Pro Val Met Leu Val Cys Gly Asp Asp Leu	286
80 85 90 95	
GTC GTC ATC TCG GAG AGC CAG GGT AAC GAG GAG GAC GAG CGA AAC CTG Val Val Ile Ser Glu Ser Gln Gly Asn Glu Glu Asp Glu Arg Asn Leu	334
100 105 110	
AGA GCT Arg Ala	340

(2) INFORMATION FOR SEQ ID NO: 216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 216:

Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Glu Ser Ile Tyr Gln
 1 5 10 15

Ala Cys Ser Leu Pro Gln Glu Ala Arg Thr Val Ile His Ser Leu Thr
 20 25 30

Glu Arg Leu Tyr Val Gly Gly Pro Met Ile Asn Ser Lys Gly Gln Ser
 35 40 45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser Met
 50 55 60

Gly Asn Thr Met Thr Cys Tyr Ile Lys Ala Leu Ala Ala Cys Lys Ala
 65 70 75 80

Ala Gly Ile Val Asp Pro Val Met Leu Val Cys Gly Asp Asp Leu Val
 85 90 95

Val Ile Ser Glu Ser Gln Gly Asn Glu Glu Asp Glu Arg Asn Leu Arg
 100 105 110

Ala

(2) INFORMATION FOR SEQ ID NO: 217:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 340 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 2..340

- (ix) FEATURE:
 - (A) NAME/KEY: mat_peptide
 - (B) LOCATION: 2..340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217:

C TCG ACT GTC ACT GAA CAG GAC ATC AGG GTG GAA GAG GAG ATA TAT 46
 Ser Thr Val Thr Glu Gln Asp Ile Arg Val Glu Glu Ile Tyr
 1 5 10 15

CAA TGC TGC AAC CTT GAA CCG GAG GCC AGG AAA GTG ATC TCC TCC CTC 94
 Gln Cys Cys Asn Leu Glu Pro Glu Ala Arg Lys Val Ile Ser Ser Leu

20

25

30

ACG GAG CGG CTT TAC TGC GGA GGC CCT ATG TTT AAC AGC AAG GGG GCC	142		
Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly Ala			
35	40	45	
CAG TGT GGT TAT CGC CGT TGC CGT GCC AGT GGA GTT CTG CCT ACC AGC	190		
Gln Cys Gly Tyr Arg Cys Arg Cys Arg Ala Ser Gly Val Leu Pro Thr Ser			
50	55	60	
TTT GGC AAC ACA ATC ACT TGT TAC ATC AAG GCC ACA ACG GCC GCG AAG	238		
Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Thr Ala Ala Lys			
65	70	75	
GCC GCA GGC CTC CGG AAC CCG GAC TTT CTT GTC TGC GGA GAT GAT CTG	286		
Ala Ala Gly Leu Arg Asn Pro Asp Phe Leu Val Cys Gly Asp Asp Leu			
80	85	90	95
GTC GTG GTG GCT GAG AGT GAT GGC GTC GAC GAG GAT AGA GCA GCC CTG	334		
Val Val Val Ala Glu Ser Asp Gly Val Asp Glu Asp Arg Ala Ala Leu			
100	105	110	
AGA GCC		340	
Arg Ala			

(2) INFORMATION FOR SEQ ID NO: 218:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 218:

Ser Thr Val Thr Glu Gln Asp Ile Arg Val Glu Glu Glu Ile Tyr Gln			
1	5	10	15
Cys Cys Asn Leu Glu Pro Glu Ala Arg Lys Val Ile Ser Ser Leu Thr			
20	25	30	
Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly Ala Gln			
35	40	45	
Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr Ser Phe			
50	55	60	
Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Thr Ala Ala Lys Ala			
65	70	75	80
Ala Gly Leu Arg Asn Pro Asp Phe Leu Val Cys Gly Asp Asp Leu Val			
85	90	95	
Val Val Ala Glu Ser Asp Gly Val Asp Glu Asp Arg Ala Ala Leu Arg			
100	105	110	

Ala

(2) INFORMATION FOR SEQ ID NO: 219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219:

Arg Ser Glu Gly Arg Thr Ser Trp Ala Gln
1 5 10

(2) INFORMATION FOR SEQ ID NO: 220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 220:

Arg Ser Glu Gly Arg Thr Ser Trp Ala Gln
1 5 10

(2) INFORMATION FOR SEQ ID NO: 221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221:

Arg Thr Glu Gly Arg Thr Ser Trp Ala Gln
1 5 10

(2) INFORMATION FOR SEQ ID NO: 222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 629 base pairs

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- (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 3..629

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION: 3..629

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 222:

TA GAC TTT TGG GAG AGC GTC TTC ACT GGA CTA ACT CAC ATA GAT GCC		47
Asp Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His Ile Asp Ala		
1 5 10 15		
CAC TTT CTG TCA CAG ACT AAG CAG CAG GGA CTC AAC TTC TCG TTC CTG		95
His Phe Leu Ser Gln Thr Lys Gln Gln Gly Leu Asn Phe Ser Phe Leu		
20 25 30		
ACT GCC TAC CAA GCC ACT GTG TGC GCT CGC GCG CAG GCT CCT CCC CCA		143
Thr Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala Pro Pro Pro		
35 40 45		
AGT TGG GAC GAG ATG TGG AAG TGT CTC GTA CGG CTT AAG CCA ACA CTA		191
Ser Trp Asp Glu Met Trp Lys Cys Leu Val Arg Leu Lys Pro Thr Leu		
50 55 60		
CAT GGA CCT ACG CCT CTT CTA TAT CGG TTG GGG CCT GTC CAA AAT GAA		239
His Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Pro Val Gln Asn Glu		
65 70 75		
ATC TGC TTG ACA CAC CCC ATC ACA AAA TAC ATC ATG GCA TGC ATG TCA		287
Ile Cys Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met Ser		
80 85 90 95		
GCT GAT CTG GAA GTA ACC ACC AGC ACC TGG GTT TTG CTT GGA GGG GTC		335
Ala Asp Leu Glu Val Thr Thr Ser Thr Trp Val Leu Leu Gly Gly Val		
100 105 110		
CTC GCG GCC CTA GCG GCC TAC TGC TTG TCA GTC GGT TGT GTT GTG ATT		381
Leu Ala Ala Leu Ala Ala Tyr Cys Leu Ser Val Gly Cys Val Val Ile		
115 120 125		
GTG GGT CAT ATC GAG CTG GGG GGC AAG CCG GCA ATC GTT CCA GAC AAA		433
Val Gly His Ile Glu Leu Gly Gly Lys Pro Ala Ile Val Pro Asp Lys		
130 135 140		

GAG GTG TTG TAT CAA CAA TAC GAT GAG ATG GAA GAG TGC TCA CAA GCT Glu Val Leu Tyr Gln Gln Tyr Asp Glu Met Glu Glu Cys Ser Gln Ala 145 150 155	479
GCC CCA TAT ATC GAA CAA GCT CAG GTA ATA GCT CAC CAG TTC AAG GAA Ala Pro Tyr Ile Glu Gln Ala Gln Val Ile Ala His Gln Phe Lys Glu 160 165 170 175	527
AAA GTC CTT GGA TTG CTG CAG CGA GCC ACC CAA CAA GCT GTC ATT Lys Val Leu Gly Leu Leu Gln Arg Ala Thr Gln Gln Ala Val Ile 180 185 190	575
GAG CCC ATA GTA ACT ACC AAC TGG CAA AAG CTT GAG GCC TTT TGG CAC Glu Pro Ile Val Thr Thr Asn Trp Gln Lys Leu Glu Ala Phe Trp His 195 200 205	623
AAG CAT Lys His	629

(2) INFORMATION FOR SEQ ID NO: 223:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223:

Asp Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His Ile Asp Ala His 1 5 10 15
Phe Leu Ser Gln Thr Lys Gln Gln Gly Leu Asn Phe Ser Phe Leu Thr 20 25 30
Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala Pro Pro Pro Ser 35 40 45
Trp Asp Glu Met Trp Lys Cys Leu Val Arg Leu Lys Pro Thr Leu His 50 55 60
Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Pro Val Gln Asn Glu Ile 65 70 75 80
Cys Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met Ser Ala 85 90 95
Asp Leu Glu Val Thr Thr Ser Thr Trp Val Leu Leu Gly Gly Val Leu 100 105 110
Ala Ala Leu Ala Ala Tyr Cys Leu Ser Val Gly Cys Val Val Ile Val 115 120 125
Gly His Ile Glu Leu Gly Gly Lys Pro Ala Ile Val Pro Asp Lys Glu 130 135 140

Val Leu Tyr Gln Gln Tyr Asp Glu Met Glu Glu Cys Ser Gln Ala Ala
145 150 155 160

Pro Tyr Ile Glu Gln Ala Gln Val Ile Ala His Gln Phe Lys Glu Lys
165 170 175

Val Leu Gly Leu Leu Gln Arg Ala Thr Gln Gln Gln Ala Val Ile Glu
180 185 190

Pro Ile Val Thr Thr Asn Trp Gln Lys Leu Glu Ala Phe Trp His Lys
195 200 205

His

(2) INFORMATION FOR SEQ ID NO: 224:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: 2..12

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224:

Ile His Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile
1 5 10

(2) INFORMATION FOR SEQ ID NO: 225:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225:

Val Asn Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile
1 5 10

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 226:

Val Asn Tyr Arg Asn Ala Ser Gly Val Tyr His Ile
1 5 10

(2) INFORMATION FOR SEQ ID NO: 227:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227:

Val Asn Tyr His Asn Thr Ser Gly Ile Tyr His Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 228:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228:

Gln His Tyr Arg Asn Ala Ser Gly Ile Tyr His Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 229:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229:

Gln His Tyr Arg Asn Val Ser Gly Ile Tyr His Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 230:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230:

Ile His Tyr Arg Asn Ala Ser Asp Gly Tyr Tyr Ile
1 5 10

(2) INFORMATION FOR SEQ ID NO: 231:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231:

Leu Gln Val Lys Asn Thr Ser Ser Ser Tyr Met Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 232:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232:

Val Trp Gln Leu Arg Ala Ile Val Leu His Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 233:

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- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233:

Val Tyr Glu Ala Asp Tyr His Ile Leu His Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 234:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 234:

Val Tyr Glu Thr Asp Asn His Ile Leu His Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 235:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 235:

Val Tyr Glu Thr Glu Asn His Ile Leu His Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 236:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 236:

Val Phe Glu Thr Val His His Ile Leu His Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 237:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237:

Val Phe Glu Thr Glu His His Ile Leu His Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 238:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238:

Val Phe Glu Thr Asp His His Ile Met His Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 239:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239:

Val Tyr Glu Thr Glu Asn His Ile Leu His Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 240:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 240:

Val Tyr Glu Ala Asp Ala Leu Ile Leu His Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO: 241:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 241:

Val Gln Asp Gly Asn Thr Ser Ala Cys Trp Thr Pro Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 242:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242:

Val Lys Thr Gly Asn Gln Ser Arg Cys Trp Val Ala Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 243:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243:

Val Lys Thr Gly Asn Gln Ser Arg Cys Trp Val Ala Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 244:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244:

Val Arg Thr Gly Asn Gln Ser Arg Cys Trp Val Ala Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 245:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245:

Val Lys Thr Gly Asn Gln Ser Arg Cys Trp Ile Ala Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246:

Val Lys Thr Gly Asn Gln Ser Arg Cys Trp Ile Ala Leu

1

5

10

(2) INFORMATION FOR SEQ ID NO: 247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247:

Val	Lys	Thr	Gly	Asn	Ser	Val	Arg	Cys	Trp	Ile	Pro	Leu
1						5				10		

(2) INFORMATION FOR SEQ ID NO: 248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248:

Val	Lys	Thr	Gly	Asn	Val	Ser	Arg	Cys	Trp	Ile	Ser	Leu
1					5					10		

(2) INFORMATION FOR SEQ ID NO: 249:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 249:

Val	Arg	Lys	Asp	Asn	Val	Ser	Arg	Cys	Trp	Val	Gln	Ile
1					5					10		

(2) INFORMATION FOR SEQ ID NO: 250:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 250:

Ala Pro Ser Phe Gly Ala Val Thr Ala Pro
1 5 10

(2) INFORMATION FOR SEQ ID NO: 251:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251:

Val Ser Gln Pro Gly Ala Leu Thr Lys Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO: 252:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252:

Val Lys Tyr Val Gly Ala Thr Thr Ala Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO: 253:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253:

Ala Pro Tyr Ile Gly Ala Pro Val Glu Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO: 254:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254:

Ala Gln His Leu Asn Ala Pro Leu Glu Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO: 255:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 255:

Ser Pro Tyr Val Gly Ala Pro Leu Glu Pro
1 5 10

(2) INFORMATION FOR SEQ ID NO: 256:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 256:

Ser Pro Tyr Ala Gly Ala Pro Leu Glu Pro
1 5 10

(2) INFORMATION FOR SEQ ID NO: 257:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 257:

Ala Pro Tyr Leu Gly Ala Pro Leu Glu Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO: 258:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258:

Ala Pro Tyr Leu Gly Ala Pro Leu Glu Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO: 259:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259:

Ala Pro Tyr Val Gly Ala Pro Leu Glu Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO: 260:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260:

Asn Val Pro Tyr Leu Gly Ala Pro Leu Thr Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO: 261:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261:

Ala Pro His Leu Arg Ala Pro Leu Ser Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO: 262:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262:

Ala Pro Tyr Leu Gly Ala Pro Leu Thr Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO: 263:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 263:

Arg Pro Arg Gln His Ala Thr Val Gln Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO: 264:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264:

Ser Pro Gln His His Lys Phe Val Gln Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO: 265:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265:

Arg Pro Arg Arg Leu Trp Thr Thr Gln Glu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 266:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266:

Pro Pro Arg Ile His Glu Thr Thr Gln Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO: 267:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267:

Thr Ile Ser Tyr Ala Asn Gly Ser Gly Pro Ser Asp Asp Lys
1 5 10

(2) INFORMATION FOR SEQ ID NO: 268:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268:

Ser Arg Arg Gln Pro Ile Pro Arg Ala Arg Arg Thr Glu Gly Arg Ser
1 5 10 15

Trp Ala Gln

(2) INFORMATION FOR SEQ ID NO: 269:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1443 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1443

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..1443

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269:

ACC ATC ACC ACC GGA GCT TCT ATC ACA TAC TCC ACT TAC GGC AAG TTC
Thr Ile Thr Thr Gly Ala Ser Ile Thr Tyr Ser Thr Tyr Gly Lys Phe

1	5	10	15	
CTT GCT GAT GGA GGG TGT TCA GGC GGC GCG TAT GAC GTG ATC ATA TGC Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp Val Ile Ile Cys				96
20	25		30	
GAC GAG TGC CAT TCC CAG GAC GCC ACC ACC ATT CTT GGG ATA GGC ACT Asp Glu Cys His Ser Gln Asp Ala Thr Thr Ile Leu Gly Ile Gly Thr				144
35	40		45	
GTC CTT GAC CAG GCA GAG ACG GCT GGA GCT AGG CTC GTC GTC TTG GCC Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu Val Val Leu Ala				192
50	55		60	
ACG GCC ACC CCT CCC GGC AGT GTG ACA ACG CCC CAC CCC AAC ATC GAG Thr Ala Thr Pro Pro Gly Ser Val Thr Thr Pro His Pro Asn Ile Glu				240
65	70		75	
GAA GTG GCC CTG CCT CAG GAG GGG GAG GTT CCC TTC TAC GGC AGA GCC Glu Val Ala Leu Pro Gln Glu Gly Glu Val Pro Phe Tyr Gly Arg Ala				288
85	90		95	
ATT CCC CTT GCT TTT ATA AAG GGT GGT AGG CAT CTC ATC TTC TGC CAT Ile Pro Leu Ala Phe Ile Lys Gly Arg His Leu Ile Phe Cys His				336
100	105		110	
TCC AAG AAA AAA TGT GAT GAA CTC GCC AAG CAA CTG ACC AGC CTG GGC Ser Lys Lys Lys Cys Asp Glu Leu Ala Lys Gln Leu Thr Ser Leu Gly				384
115	120		125	
GTG AAC GCC GTG GCA TAT TAT AGA GGT CTA GAC GTC GCC GTC ATC CCC Val Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val Ala Val Ile Pro				432
130	135		140	
ACA GCA GGA GAC GTG GTC GTG TGC AGC ACC GAC GCG CTC ATG ACG GGA Thr Ala Gly Asp Val Val Val Cys Ser Thr Asp Ala Leu Met Thr Gly				480
145	150		155	
160				
TTC ACC GGC GAC TTT GAT TCT GTC ATA GAC TGC AAC TCC GCC GTC ACT Phe Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn Ser Ala Val Thr				528
165	170		175	
CAG ACG GTG GAC TTC AGT CTG GAT CCC ACT TTT ACC ATT GAG ACT ACC Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr Ile Glu Thr Thr				576
180	185		190	
ACA GTG CCC CAG GAC GCA GTG TCC AGA AGC CAG CGT AGG GGC CGC ACG Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg Arg Gly Arg Thr				624
195	200		205	
GGG AGA GGT AGG CAC GGC ATA TAC CGG TAT GTC TCG GCT GGA GAG AGA Gly Arg Gly Arg His Gly Ile Tyr Arg Tyr Val Ser Ala Gly Glu Arg				672
210	215		220	
CCG TCT GAC ATG TTC GAC TCC GTG GTG CTC TGT GAG TGC TAC GAT GCC Pro Ser Asp Met Phe Asp Ser Val Val Leu Cys Glu Cys Tyr Asp Ala				720
225	230		235	
				240

GGA TGT GCG TGG TAT GAT CTG ACT CCT GCC GAG ACT ACC GTG AGG TTG Gly Cys Ala Trp Tyr Asp Leu Thr Pro Ala Glu Thr Thr Val Arg Leu 245 250 255	763
CGC GCT TAC ATA AAC ACC CCC GGG CTC CCT GTC TGT CAG GAC CAT TTG Arg Ala Tyr Ile Asn Thr Pro Gly Leu Pro Val Cys Gln Asp His Leu 260 265 270	816
GAA TTC TGG GAG GGG GTG TTC ACG GGG CTC ACT AAC ATC GAC GCT CAC Glu Phe Trp Glu Gly Val Phe Thr Gly Leu Thr Asn Ile Asp Ala His 275 280 285	864
ATG CTG TCA CAG ACC AAA CAG GGT GGG GAG AAT TTC CCA TAC CTT GTA Met Leu Ser Gln Thr Lys Gln Gly Glu Asn Phe Pro Tyr Leu Val 290 295 300	912
CGC TAC CAA GCA ACA GTC TGT GTT CGC GCG AAA GCG CCC CCC CCC AGC Ala Tyr Gln Ala Thr Val Cys Val Arg Ala Lys Ala Pro Pro Pro Ser 305 310 315 320	960
TGG GAC ACA ATG TGG AAA TGC ATG CTC CGT CTC AAA CCG ACT TTA ACT Trp Asp Thr Met Trp Lys Cys Met Leu Arg Leu Lys Pro Thr Leu Thr 325 330 335	1008
GGC CCT ACT CCC CTC TTG TAC AGG CTG GGG CCC GTC CAG AAT GAG ATC Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Pro Val Gln Asn Glu Ile 340 345 350	1056
ACA CTG ACG CAC CCC ATC ACC AAG TAC ATT ATG GCT TGC ATG TCT GCG Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met Ser Ala 355 360 365	1104
GAC TTG GAG GTC ATT ACC AGC ACT TGG GTT CTG GTG GGG GGC GTT GTG Asp Leu Glu Val Ile Thr Ser Thr Trp Val Leu Val Gly Val Val 370 375 380	1152
GCG GCC CTG GCG GCC TAC TGC TTG ACG GTG GGT TCG GTA GCC ATA GTC Ala Ala Leu Ala Ala Tyr Cys Leu Thr Val Gly Ser Val Ala Ile Val 385 390 395 400	1200
GGT AGG ATC ATC CTC TCT GGG AAA CCT GCC ATC ATT CCC GAT AGG GAG Gly Arg Ile Ile Leu Ser Gly Lys Pro Ala Ile Ile Pro Asp Arg Glu 405 410 415	1248
GCA TTA TAC CAG CAA TTT GAT GAG ATG GAG GAG TGC TCG GCC TCG TTG Ala Leu Tyr Gln Gln Phe Asp Glu Met Glu Glu Cys Ser Ala Ser Leu 420 425 430	1296
CCC TAT ATG GAC GAG ACA CGT GCC ATT GCC GGA CAA TTC AAA GAG AAA Pro Tyr Met Asp Glu Thr Arg Ala Ile Ala Gly Gln Phe Lys Glu Lys 435 440 445	1344
GTG CTC GGC TTC ATC AGC ACG ACC GGC CAG ARG GCT GAA ACT CTG AAG Val Leu Gly Phe Ile Ser Thr Thr Gly Gln Lys Ala Glu Thr Leu Lys 450 455 460	1392
CCG GCA GCC ACG TCT GTG TGG AAC AAG GCT GAG CAG TTC TGG GCC ACA Pro Ala Ala Thr Ser Val Trp Asn Lys Ala Glu Gln Phe Trp Ala Thr 465 470 475 480	1440

TAC
Tyr

1443

(2) INFORMATION FOR SEQ ID NO: 270:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 481 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

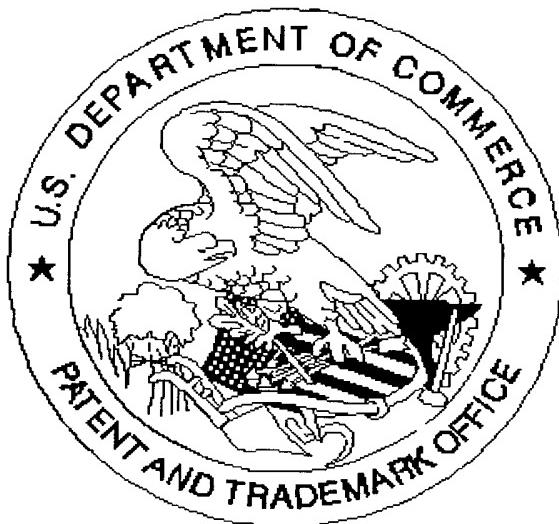
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270:

Thr	Ile	Thr	Thr	Gly	Ala	Ser	Ile	Thr	Tyr	Ser	Thr	Tyr	Gly	Lys	Phe	
1				5					10					15		
Leu	Ala	Asp	Gly	Gly	Cys	Ser	Gly	Gly	Ala	Tyr	Asp	Val	Ile	Ile	Cys	
					20				25					30		
Asp	Glu	Cys	His	Ser	Gln	Asp	Ala	Thr	Thr	Ile	Leu	Gly	Ile	Gly	Thr	
					35			40					45			
Val	Leu	Asp	Gln	Ala	Glu	Thr	Ala	Gly	Ala	Arg	Leu	Val	Val	Leu	Ala	
					50			55					60			
Thr	Ala	Thr	Pro	Pro	Gly	Ser	Val	Thr	Thr	Pro	His	Pro	Asn	Ile	Glu	
					65			70			75			80		
Gl	u	Val	Ala	Leu	Pro	Gln	Glu	Gly	Glu	Val	Pro	Phe	Tyr	Gly	Arg	Ala
					85				90					95		
Ile	Pro	Leu	Ala	Phe	Ile	Lys	Gly	Arg	His	Leu	Ile	Phe	Cys	His		
					100			105					110			
Ser	Lys	Lys	Lys	Cys	Asp	Glu	Leu	Ala	Lys	Gln	Leu	Thr	Ser	Leu	Gly	
					115			120					125			
Val	Asn	Ala	Val	Ala	Tyr	Tyr	Arg	Gly	Leu	Asp	Val	Ala	Val	Ile	Pro	
					130			135			140					
Thr	Ala	Gly	Asp	Val	Val	Val	Cys	Ser	Thr	Asp	Ala	Leu	Met	Thr	Gly	
					145			150			155			160		
Phe	Thr	Gly	Asp	Phe	Asp	Ser	Val	Ile	Asp	Cys	Asn	Ser	Ala	Val	Thr	
					165				170					175		
Gln	Thr	Val	Asp	Phe	Ser	Leu	Asp	Pro	Thr	Phe	Thr	Ile	Glu	Thr	Thr	
					180			185					190			
Thr	Val	Pro	Gln	Asp	Ala	Val	Ser	Arg	Ser	Gln	Arg	Arg	Gly	Arg	Thr	
					195			200			205					
Gly	Arg	Gly	Arg	His	Gly	Ile	Tyr	Arg	Tyr	Val	Ser	Ala	Gly	Glu	Arg	
					210			215			220					
Pro	Ser	Asp	Met	Phe	Asp	Ser	Val	Val	Leu	Cys	Glu	Cys	Tyr	Asp	Ala	

292

225 230 235 240
Gly Cys Ala Trp Tyr Asp Leu Thr Pro Ala Glu Thr Thr Val Arg Leu
245 250 255
Arg Ala Tyr Ile Asn Thr Pro Gly Leu Pro Val Cys Gln Asp His Leu
260 265 270
Glu Phe Trp Glu Gly Val Phe Thr Gly Leu Thr Asn Ile Asp Ala His
275 280 285
Met Leu Ser Gln Thr Lys Gln Gly Gly Glu Asn Phe Pro Tyr Leu Val
290 295 300
Ala Tyr Gln Ala Thr Val Cys Val Arg Ala Lys Ala Pro Pro Pro Ser
305 310 315 320
Trp Asp Thr Met Trp Lys Cys Met Leu Arg Leu Lys Pro Thr Leu Thr
325 330 335
Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Pro Val Gln Asn Glu Ile
340 345 350
Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met Ser Ala
355 360 365
Asp Leu Glu Val Ile Thr Ser Thr Trp Val Leu Val Gly Gly Val Val
370 375 380
Ala Ala Leu Ala Ala Tyr Cys Leu Thr Val Gly Ser Val Ala Ile Val
385 390 395 400
Gly Arg Ile Ile Leu Ser Gly Lys Pro Ala Ile Ile Pro Asp Arg Glu
405 410 415
Ala Leu Tyr Gln Gln Phe Asp Glu Met Glu Glu Cys Ser Ala Ser Leu
420 425 430
Pro Tyr Met Asp Glu Thr Arg Ala Ile Ala Gly Gln Phe Lys Glu Lys
435 440 445
Val Leu Gly Phe Ile Ser Thr Thr Gly Gln Lys Ala Glu Thr Leu Lys
450 455 460
Pro Ala Ala Thr Ser Val Trp Asn Lys Ala Glu Gln Phe Trp Ala Thr
465 470 475 480
Tyr

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